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                                                                                                                  SerMetGladenCysGlyCysGlnProdenValCysCysGysSerLysPheGlyTyrCysGly
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14-MAR-2003; 2003US-00389432.
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                                                               ATGAACAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCGCCCACCATCAGGGCCATCAAC
New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                                                                                               Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
                                                                                                                                                  ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                   Chitinase variant polynucleotide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PION-) PIONEER HI-BRED INT INC
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96.76%
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14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                     ADS92687 standard; DNA; 774
                                                                                                                                                                                                                                                                                          (first entry)
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P-PSDB; ADS92688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VERD-) VERDIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                             Heterodera
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                                                                                                                                                                      221 GlyalaLeuGluCygAanGlyAanAanProAlaGlnMetAanAlaArgValGlyTyrTyr
                                                                                                                                                                                                                                          161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly
                                  478 ATCTCGTGGAACTACAACTACGGGCCCGCGGGAGGGCCATCGGCTTCGACGGGCTCGGG
                                                                        AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp
                                                                                                          538 GACCCCGGCAGGCTGGCGCGGGACGCCGTGGTGGCGTTCAAGGCGGCGCCCTCTGGTTCTGG
                                                                                                                                               MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn
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                                                                                                                                                                                                                                                                                          241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                                                                                                                                                               Sequence 774 BP; 139 A; 249 C; 282 G; 104 T; 0 U; 0 Other;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AcGACCGACGCCTACTGCGGCGACGGTGCCAGTCGGCCCGTGCCGCTCG---GGCGGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 GGTGGCGGCGGTGGCGGCGGAGGCGGGAGGCAGTGGCGGTGCGAACGTGGCTAATGTG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GTCACCGACGCGTTCTTCAACGCCATCAAGAACCAGGCCGGGAGCGGGGGGGAGGGCAAG 237
                                                                                                                                                                                                                                                                                                                                                                 encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Pusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                The invention relates to chitinase polypeptides and the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCGATGCAGAACTGCGGCTGCCAGCCAAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC
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                                                                                                                                                                                                                                                      New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 59; 197pp; English.
                                                                                                                                                              Simmons CR,
                                                                                                       (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC.
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                                22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
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22-OCT-2003; 2003WO-US033588
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1382.50
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P-PSDB; ADS92682.
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                                                                                                                                      ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly
                                                                                                                                                                                                                                                                                                                  ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys
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Conservative:
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                                                                               (1-774)
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                                                                                US-10-692-367-12 (1-257) x ADS92661
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 Percent Similarity:
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                                                                                                              The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polymucleotide of the invention.
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New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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                                                                           Claim 4; SEQ ID NO 65; 197pp; English
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                    ACCAAGAGGCAGTGGCCGTGCGCGGGGGCAGAACTACTACGGCGTGGCCCGCTGCAG 480
                                                lleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlalleGlyPheAspGlyLeuGly 180
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        ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyBroLeuGln
                                                             ATCTCGTGGAACTACAACTACGGGCCCGCGGGGGGGGGCCCATCGGCTTCGACGGGCTCGCC
                                                                                         AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp
                                                                                                     New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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P-PSDB; ADS92678.
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| IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
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GGCGGGTCACAGGTGCAGGGCAAGCGCGAGATCGCCGCCTTCTTCGCGCATGTCACGCAC 357
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                                                                                                                                                                                                                                                                                                                                                                         MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrlleArgAlalleAsn
                                                ThrivsArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln
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                                 GluThrGlyHisPheCysTyrlleSerGluValAsnLysSerAsnAlaTyrCysAspPro
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(PION-) PIONEER HI-BRED INT INC
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                       ds; plant resistance; fungus; nematode; Fusarium;
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enha plant resistance to a fungus or nematode. This sequence represents chitinase variant polynucleotide of the invention.
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Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
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(PION-) PIONEER HI-BRED INT INC
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The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                           gene; ds; plant resistance; fungus; nematode; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 774 BP; 145 A; 251 C; 276 G; 102 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 37; 197pp; English.
                                                                                                                                                                                                                          Chitinase variant polynucleotide #16.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                          ADS92653 standard; DNA; 774
                                                                                                                                                                         (first entry)
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P-PSDB; ADS92654.
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Heterodera.
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                                   241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys
                                                        Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                   Chitinase variant polynucleotide #19
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
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                                                                                   The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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        New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                    Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;
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                                                         Claim 4; SEQ ID NO 67; 197pp; English
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                                                    GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
                                                       340 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCCTACTGCGACCCG 399
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Search completed: May 23, 2005, 17:44:53 Job time : 385.684 secs

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MZECHITA 843 bp DNA linear PLN 27-APR-1993
Zea mays chitinase A (seed chitinase) gene, complete cds.
M84164
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1 (bases 1 to 843)

Huynh, Q. K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.
Antifungal proteins from plants: Purification, molecular cloning, and antifungal properties of chitinases from maize seed J. Biol. Chem. 267 (10), 6635-6640 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Zea mays (library: Lamda GT 10 corn seed (imbibed)) seed DNA.
AY532775

AY532766

AY532783

AY532783

AY532783

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AY532787

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/db_xref="texon:4577"
/tissue_type="seed"
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AY532725
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-Q=/cgn2_1/USPTO spool/US10692367/runat_20052005_172254_20002/app_query.fasta_1.846
-Q=/cgn2_1/USPTO spool/US10692367/runat_20052005_172254_20002/app_query.fasta_1.846
-DB=GenEmbl -QPFWT=fastap -SUPFYX=rge -MINNATCH=0.1 -LAOPCIA.0 -LAOPEXX=0
-UNITS=bits -START=1 -END=-1 -MATIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10692367 @CGN 1 1 3055 @runat_20052005 172254_20002 -NCFU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES= O -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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M84165 Zea mays ch
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1 SMQNCGCQPNVCCSKFGYCG......GYYRQYCRQLGVDPGNNLTC
                                                                        May 23, 2005, 15:37:22 ; Search time 3056.63 Seconds
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                    nucleic search, using frame_plus_p2n model
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Maize chitinases and their use in enhancing disease resistance
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                            CAGAACTIGCGGCTGCCAGCCAAACGTCTGCTGCAGCAAGTTCGGCTACTGCGGGCACGACCC
                                                                                                                                                                                                                                                                                                                                         GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
                                                                                                                                   23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGly
                                                                                                                                                                        AspAlaPhePheAsnGly1leLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                 347 TACACCCGGAGTGCGTTCCTGAGGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCGTAAGTTGGCTCGGTCTTCCGCGCGCCGCAGGTTCTTTGATTTTAATTTGACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyHis-PheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLy
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                                                                                                                                                                                                                                                                                                                                                                                                        TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATGCTGATCAAATTATTTTTTTTTGGAAAATTTTTCCGCTGCTGTGTCTGTGTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCAGTGGCCCGCGGGGCAGAAGTACTACGGGCGCGCCCGCTGCAGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPr
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VVAFKAALWFWNNSVHGVVPQGFGATTRAINGALECGGNNPAQWNARVGYYRQYCRQI
GVDPGPNLTC"
                                                                                                                                                                                                                                                                                                                                                                                                   linear PLN 29-JUL-2004 (chiB) gene, complete cds.
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Sea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1128)
Tiffin, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (33-JAN-2004) Plant Biology, University of Minnesota,
1445 Gorner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. 1128
/organism="Zea diploperennis"
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                                                                                   AsnValHisArgValMetProGlnGlyPheGlyAlaThrlleArgAlaIleAsnGlyAla
                                                                                                                                 Agograciosogracios de segon de contra de contra
                                                                                                                                                                             LeuGluCysAsnAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Zea diploperennis isolate d6 chitinase
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/gene="chiB"
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Genetics 167 (3), 1331-1340 (2004)
15280246
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join(14. .470,592. .995)
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81.76%
78.72%
88.91%
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Tiffin, P.
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Query Match:
DB:
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AY532740
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642 222 702

522 182 582 242

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ALMFWMNNYHRLMPQGFGATIRAINGALECNGNNPAQMNARVGYXKQYCQQLRVDGP
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gene,
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kukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Direct Submission
Submitted (23.JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. 1094
                                                                                                                                                                                                                                                                          223 LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln
TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro
                                                                                                                                                          203 AsnvalHisArgvalMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla
                                                                                                                                      GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn
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/gene="chiA"
/codon_start=1
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/gene="chiA"
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Tiffin, P.
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 810)

Huynh, Q.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.

Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed J. Biol. Chem. 267 (10), 6635-6640 (1992)
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                                                                                                                                                                             corn seed
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Matches:
Conservative:
Mismatches:
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gene,
                                                                                                            Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermarophyta, Magnoliophyta, Lillopsida, Poales, Poaceae; PACCAD
clade; Panicoideae, Andropogoneae; Zea.
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join(<14 ..45,579. .>982)
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1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Mismatches:
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/db_xref="taxon:76912"
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/gene="chiA"
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Zea mays subsp. parviglumis
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. .1131
                                                        TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly
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Zea mays subsp. parviglumis isolate pl chitinase (chiA) gene,
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Sea mays subsp. parviglumis
Bukaryota; Unidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1115)
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                      AlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHis
                                                                                                                                                 ArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCye
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CCGTGCGCGCGGCGGAGAAGTACTACGGCGCGCGCCCGCTGCAGATCTCGTGGAACTAC
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/mol_type="genomic DNA"
/culfivar="P1384070"
/isolate="pl"
/sub_species="parviglumis"
/db_xref="taxon:76912"
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/gene="chiA"
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Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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          TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly
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(chiA) gene,
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Submitted (23-JAN-2004) Plant Biology, University
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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/organism="Zea diploperennis"
/mol_type="genomic DNA"
/cultivar="M005"
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                                                            Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Sukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Tiffin,P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, '1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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230
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Genetics 167 (3), 1331-1340 (2004)
15280246
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gene="chiB"
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Tiffin, P.
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  DEFINITION
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AUTHORS
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complete cds.
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                                                                             210 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCyBAsnGlyAsnAsn
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GCCGGGAGGGACATCGGCTTCAACGGGCTCGCCGACCCCCAACAGGGTGGCGCAGGACGCC
                           ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro
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Zea diploperennis isolate d3 chitinase (chiA) gene,
AYS32783
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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Conservative:
Mismatches:
Indels:
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join (<24. .450,550. .>953)
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Genetics 167 (3), 1331-1340 (2004) 15280246
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Zea diploperennis
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Best Local Similarity:
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Conservative:
Mismatches:
Indels:
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                    Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspalaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe
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                                                                   histories of chitinase genes in
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Matches:
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Mismatches:
Indels:
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Genetics 167 (3), 1331-1340 (2004)
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join(24. .450,550. .953)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1110)
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Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                   GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro
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clade, Panicoideae, Andropogoneae, Zea.
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WMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYKQYCQQLRVDFGPNITC
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Direct Submission
Submitted (13-JAN-2004) Plant Biology, University of 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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PLN 29-JUL-2004 complete cds.

Query Match: DB:

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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Tomparative evolutionary histories of chitinase genes in the genus

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E cologonose in Frontinase activity; IEA.

E cologonose in Prontinase activity; IEA.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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llarity 91.8%; Pred. No. 4e-89;
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ProDom; PD34900; Glyco_hydro_19; 1.

BNART; SM00270; ChtBD1; 1.

PROSITE; PS00773; CHITINASE 19 1; 1.

PROSITE; PS00773; CHITINASE 19 1; 1.

PROSITE; PS00076; CHITINASE 19 2; 1.

PROSITE; PS00026; CHIT BIND 1 1; 1.

Chitin-binding.

Chitin-binding.
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
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183 GRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAOMNARVGYYRQ 242
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InterPro; IPR001002; Chitin binding_1.
InterPro; IPR001002; Chitin binding_1.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00182; Chitin bind_1; 1.
PRINKTS; PR00451; CHTTINBINDNG.
ProDom; PD000609; Chitin binding_1; 1.
PROSITE; PS00026; CHIT BIND_11; 1.
PROSITE; PS00026; CHIT_BIND_11; 1.
PROSITE; PS00073; CHIT_BIND_12; 1.
PROSITE; PS00773; CHIT_BIND_12; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
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                          GHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDP 182
                                                                         GRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYRQ 242
                                                                                        212 GRVARDAVVAFKAALWFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQ 271
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  GSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHET 151
                                         26 QNCGCQPNFCCSKFGYCGTIDAYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGGGGGGANVANVT
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                                                                                                                                                                                                                                                                                            Zea mays (subsp. parviglumis) (Balsas teosinte).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD Clade; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 0008568; F: chitin binding; IEA.

R GO; GO: 00016998; P: cell wall catabolism; IEA.

R GO; GO: 00016998; P: cell wall catabolism; IEA.

R GO; GO: 00006013; P: cell wall catabolism; IEA.

R InterPro; IPRO01002; P: chitin binding 1.

R InterPro; IPRO01002; Chitin binding 1.

R PRINTS; PRO041; Glyco_Hydro_19; 1.

R PRINTS; PRO041; Glyco_Hydro_19; 1.

R PRODM; PD354900; Chitin binding 1; 1.

R PROMOTO; ChtBD1; 1.

R PROSITE; PS00774; CHITINASE 19; 1.

R PROSITE; PS00774; CHITINASE 19; 1.

R PROSITE; PS00026; CHIT_BIND_1; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 280 AA; 29253 MW; 4FC5AABD08ED6671 CRC64;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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                                                                                                                                                                                                           280 AA
                                                                                                                                                                                                                                   Created)
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Genetics 167:1331-1340(2004).
EMBL; AYS32775; ART40044.1; -
HSSP; P10969; 1K7V.
                                                                                                                                                                                                                                (TrEMBLrel. 27, CTEMBLrel. 27, I
                                                                                                                         243 YCRQLGVDPGNNLTC 257
                                                                                                                                                272 YCROLGVDPGPNLTC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.24
Matches 230; Conservative
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=76912;
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                                                                                                                                                                                                                                                                      Chitinase.
Name=chiA;
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Облвке;
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
206 NRVAQDAVIAFKTALWFWMNNVHRLMPQGFGATIRAINGALECNGNNPAQMNARVGYKQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92156129; PubMed=1740436;
Verburg J.G., Smith C.E., Lisek C.A., Huynh Q.K.;
"Identification of an essential tyrosine residue in the catalytic site of a chitinase isolated from Zea mays that is selectively modified during inactivation with 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the glycosyl hydrolase 19 family. Chitinase class I subfamily.
-!- SIMILARITY: Contains 1 chitin-binding type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92202208; PubMed=1551872;
Huynh Q.K., Hironaka C.M., Levine B.B., Smith C.E., Borgmeyer J.R.,
Shah D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.
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--- FUNCTION: This protein functions as a defense against chitin containing fungal pathogens.
--- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of Nacetyl-D-glucosamine polymers of chitin.
--- MISCELLANBOUS: Maize chitinase B seems to be less active than
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A)
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63 DAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATHET 122
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                                                                                                                                                                                                                                                                                                                   32 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGG------GGANVASVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 GHFCYISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays (subsp. parviglumis) (Balsas teosinte).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                      90.6%; Score 1316; DB 2; Length 280; 91.0%; Pred. No. 2.9e-87; ive 8; Mismatches 9; Indels
                                                                                                                                                                                     280 AA; 28963 MW; 60FA617488839998 CRC64;
     PRINTS; PRO0451; CHITINBINDNG.
ProDom; PD000609; Chitin binding_1; 1.
PRODOM; PD354900; Glyco_Fydro_19; 1.
SWART; SW00270; ChtBD1, 1.
PROSITE; PS00773; CHITINASE DEHVER GLU; UNKNOWN_1.
PROSITE; PS00774; CHITINASE 19_2; 1.
PROSITE; PS00076; CHITINASE 19_2; 1.
PROSITE; PS00026; CHIT BIND_1 1; 1.
Chitin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6JBQ9;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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GO: 000000001; F:chitin binding; IEA.
GO: 00004568; F:chitinase activity; IEA.
GO: 00101698; F:chitinase activity; IEA.
GO: 0010000012; F:chitin catabolism; IEA.
GO: 001000013; P:chitin catabolism; IEA.
GO: 00100013; P:chitin catabolism; IEA.
INTERPO: IPRO1002; Chitin Linding 1.
INTERPO: IPRO1002; Chitin Linding 1.
INTERPO: IPRO1002; Glyco hydro 19.
PFODOM; PRO0018; Glyco hydro 19; 1.
ProDom; PD000009; Chitin binding 1; 1.
ProDom; PD354900; Chitin binding 1; 1.
SWART; SM00270; ChtBD1; 1.
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Genetics 167:1331-1340(2004).
BEMBL; AYS12731; AAT40000.1; -.
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gradation; Chitin-binding; Direct protein sequencing;

l 25 Multigene family; Signal.

26 20 Endochitinase A.

26 60 Chitin-binding type-1.

61 77 Hinge region (poly-Gly).

78 28 36 By similarity.

28 36 By similarity.

53 58 By similarity.

53 58 By similarity.

100 149 By similarity.

110 By similarity.

28 By similarity.
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GO; GO:0004568; Frchitinase activity; IEA.
GO; GO:0004568; Frchitinase activity; IEA.
GO; GO:0006032; Prchitinase actabolism; IEA.
GO; GO:0006032; Prchitin catabolism; IEA.
GO; GO:0009613; Presponse to pest, pathogen or parasite; IEA.
InterPro; IPR002086; Aldehyd dehydrog.
InterPro; IPR001025; Chitin Binding_1.
InterPro; IPR001025; Chitin Binding_1.
Pfem; PF00182; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                         90.9%; Score 1320; DB 1; Length 280; 90.2%; Pred. No. 1.5e-87; ive 9; Mismatches 16; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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Matches 230; Conservative
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161
248
280 AA;
         Chitin degradation;
                         Glycosidase;
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Q6JBQ2;
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145

62 85 242

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Gaps

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208 GRVARDAVVAFKAALMFWMNSVHGVVPQGFGATTRAINGALECGGNNFAQMNARVGYYRQ 267
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Tromparative evolutionary histories of chitinase genes in the genus

Tromparative evolutionary histories of chitinase genes in the genus

Tromparative evolutionary histories of chitinase genes in the genus

R. Genetics 167:131-1340(2004).

EMBL; AY53726; AAT39995.1; -.

EGO; GO:000961; F:chitin binding; IEA.

GO; GO:0004569; P:chitin catabolism; IEA.

GO; GO:0005603; P:chitin catabolism; IEA.

GO; GO:0005603; P:chitin binding.].

EMBL; PEO0102; Glyco. Indro. Indro. II.

EMBL; PEO0122; Glyco. Indro. II.

EMBL; PEO0125; Glyco. Indro. II.

EMBL; PEO0105; CHITINBINDG.

EMBL; PEO0070; CHEBD; I.

EMBL; PEO0070; CHEBD; I.

EMBL; PEO0070; CHEBD; I.

EMBL; PEO0070; CHEBD; I.

EMBL; PEO0070; CHITINASE. II.

EMBL; PEODO090; CHITINASE. II.

EMBL; PEODO090; CHITINASE. II.

EMBL; PEODO090; CHITINASE. II.

EMBL; PEODO090; CHITIN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                            Length 282;
                        Chitin-binding. _ _ _ SEQUENCE 282 AA; 29147 MW; 4E10632A4F979D20 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
                                                                                                            Query Match 90.4%; Score 1313; DB 2; Best Local Similarity 91.0%; Pred. No. 4.8e-87; Matches 232; Conservative 7; Mismatches 10;
PROSITE; PS50941; CHIT_BIND_I_2; 1.
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Q6JBQ7;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 0008568; F: chitin binding; IEA.

R GO; GO: 00016998; P: chitinase activity; IEA.

R GO; GO: 00016998; P: cell wall catabolism; IEA.

R GO; GO: 0006919; P: cell wall catabolism; IEA.

R GO; GO: 0009613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IPR001002; Chitin Binding.

R InterPro; IPR001002; Chitin Binding.

R ProDom; PRO01659; Chitin binding.

R PRIMYS; PR00451; CHITINBINGNG.

R PRODOM; PD000609; Chitin binding.

R PRODOM; PD000609; Chitin binding.

R PROSITE; PS00687; ALDEHVDE DEHYDR GLU; UNKNOWN.

R PROSITE; PS000267; ALDEHYDR.

R PROSITE; PS00026; CHIT.BIND.1.

R PROSITE; PS00026; CHIT.BIND.1.

R PROSITE; PS00026; CHIT.BIND.1.1; 1.
                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                               Query Match 90.6%; Score 1316; DB 2; Length 284; Best Local Similarity 90.6%; Pred. No. 2.9e-87; Matches 231; Conservative 10; Mismatches 12; Indels
                                 PROSITE; PS00773; CHITINASE 19_1; 1.

PROSITE; PS00774; CHITINASE 19_2; 1.

PROSITE; PS00026; CHIT BIND 1 1; 1.

CHITINIO 1 2; 1.

Chitin-binding.

SEQUENCE 284 AA; 29256 MW; B210EB7C204A6557 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chitinase.
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
         ALDEHYDE DEHYDR GLU; UNKNOWN 1
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   PS00687; ALDEHYDE DEHYDR GLK
PS00773; CHITINASE 19 1; 1.
PS000774; CHITINASE 19 2; 1.
PS00026; CHIT BIND I 1; 1.
PS50941; CHIT_BIND_I 2; 1.
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Genetics 167:1331-1340(2004).
EMBL; AY532730; AAT39999.1; -.
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206 NRVAQDAVIAFKTALMFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYKQ 265
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                                                                                             86 DAPFNGIKNQAGSGCEGKNPYTRSAFLSAVNAYPGPAHGGTEVEGKREIAAFFAHVTHET
                                                                                                                                                                         GHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDP
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                                                                DAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVBRKREIAAFFAHATHET
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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9; Mismatches 13
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Genetics 167.1331-1340(2004).
EMBL: AYS32780; AAT40049.1;
HSSP; P10969; 1K7V.
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Matches 230; Conservative
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                                                                                                                                                                   32 ÓNCGCOPNYCCSKFGYCGTTDBYCGDGCOSGPCRSGGGGGGGGGGG-----GGANVASVYT 85
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 0004568; F: chitin binding; IEA.

R GO; GO: 0004568; F: chitinase activity; IEA.

R GO; GO: 0006598; P: cell wall catabolism; IEA.

R GO; GO: 0006613; P: cell wall catabolism; IEA.

R GO; GO: 0009613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IPRO01002; Chitin binding 1.

R PRINTS; PRO0451; Glyco hydro 19.

R PRINTS; PRO0451; GHITINBINDNG;

R PRODM; PD504609; Chitin binding 1; 1.

R PRODM; PD54900; Glyco hydro 19; 1.

R PROSTITE; PS00773; CHITINASE 19 1; 1.

R PROSITE; PS00774; CHITINASE 19 1; 1.

R PROSITE; PS00774; CHITINASE 19 1; 1.

R PROSITE; PS00774; CHITINASE 19 1; 1.

R PROSITE; PS00775; CHITINASE 19 1; 1.

R PROSITE; PS00775; CHITINASE 19 1; 1.
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                                                       9; Indels
     Length
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SEOUENCE 280 AA; 29256 MW; DC908138098DE0A3 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
     DB 2;
     Score 1312; DB 2;
Pred. No. 5.6e-87;
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                                                       9; Mismatches
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Genetics 167:1331-1340(2004).
EMBL; AY532774; AAT40043.1; --
HSSP; P10969; 1K7V.
  90.4%;
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                                                          231; Conservative
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Query Match
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Matches 231
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GRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYRQ
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GO; GO: 0004568; F: chitin binding; IEA.

GO; GO: 0004568; F: chitinse activity; IEA.

GO; GO: 0005613; P: chitin catabolism; IEA.

GO; GO: 0009613; P: chitin catabolism; IEA.

GO; GO: 0009613; P: chitin catabolism; IEA.

GO; GO: 0009613; P: response to pest, pathogen or para; InterPro; IPR001002; Chitin binding_1.

InterPro; IPR001002; Chitin binding_1.

PERM: PRO0182; Glyco hydro_19.

ProDom; PD000669; Chitin binding_1; 1.

ProDom; PD000669; Chitin binding_1; 1.

SWART; SW00270; ChEBD1; 1.

SWART; SW00270; ChEBD1; 1.

RROSITE; PS000773; CHITINASE_19_1; 1.

PROSITE; PS000773; CHITINASE_19_1; 1.

RROSITE; PS000774; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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                                                                                                                                                                                                                                                             282 AA
                                                                                              243 YCRQLGVDPGNNLTC 257
                                                                                                                        Matches 230; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
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05-JUL-2004 (
05-JUL-2004 (
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Q6JBQ6
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                                                                                                                        203 NRVAQDAVIAFKTALMFWANNVHRVMPQGFGATIRAINGALBCNGNNPAQMNARVGYYKQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DAFFNGIKNQAGSGCEGKNPYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATHET 122
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                               32 QNCGCQPNVCCSKFGXCGTTDEYCGDGCQSGPCRSGGGGGSSGG-----GGANVASVVT
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                                                                                                GRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYRQ
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Genetics 167:1331-1340(2004).
EMBL; 487537733; AAT40002.1; -.
HSSP; P10969; 187V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD cladé; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 00004568; F: chitin binding; IEA.

R GO; GO: 00016598; P: chitinase activity; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

GO; GO: 00006032; P: chitin catabolism; IEA.

R InterPo; IPR001002; P: chitin catabolism; IEA.

R InterPo; IPR001002; Chitin Dinding 1.

R InterPo; IPR001002; Glyco_hydrog.

R InterPo; IPR001002; Glyco_hydrog.

R PRINTS; PR001451; CHITINBINDNG.

R ProDom; PD154900; Glyco_hydro_19; 1.

R PROSITE; PS00607; Chitin binding_1; 1.

R PROSITE; PS000687; ALDEHYDE DEHYDR_GLU; UNKNOWN 1.

R PROSITE; PS00074; CHITINBASE 19 1; 1.

R PROSITE; PS00026; CHIT_BIND_1 1; 1.
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SROHENCE 280 AA; 28993 MW; 7E6E2DA395C32FDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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Matches 231; Conservative
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206 GRVARDAVVAFKAALMFWANSVHGVVPQGFGATTRAINGALECGGNNPAQWNARVGYYRQ 265
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"Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
GENBL; AYS32727; AAT3996.1; -.
HSSP; P10969; 1K7V.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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"Comparative evolutionary histories of chitinase genes in the genus T = Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";

"L Genetics 167:1331-1340(2004).

"R EMBL; AY532768; AAT40037.1; -.

"R MSSP; P10969; LK7V.

"R GO; GO:0000661; F:chitin binding; IEA.

"GO; GO:0000662; F:chitin binding; IEA.

"GO; GO:0000632; P:chitin catabolism; IEA.

"GO; GO:0000632; P:chitin catabolism; IEA.

"GO; GO:0000603; P:chitin binding_1.

"R GO; GO:0000603; P:chitin binding_1.

"R FROM:"

"R FROM:"

"R FROM:"

"R FROM:"

"R FROM:"

"R PROSITE; PRO0702; Chitin binding_1; 1.

"R PROSITE; PRO0703; CHITINASE_19_2; 1.

"R PROSITE; PRO0704; CHITINASE_19_2; 1.

"R PROSITE; PRO0705; CHITINASE_19_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays (subsp. parviglumis) (Balsas teosinte).
Wataryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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9; Mismatches 15; Indels
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SEQUENCE 278 AA; 29127 MW; A17DF4E6B0F5FA0D CRC64;
                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
                                   268 YCRQLGVDPGPNLTC 282
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Matches 229; Conservative
YCRQLGVDPGNNLTC
                                                                                                                                                                                                                                     PRELIMINARY;
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Name=chiA;
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243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 NRVAQDAVIAFKTALMFWANNVHRVMPQGFGATIRAINGALECNGNNFAQMNARVGYYKQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
                                                                                                                                                                                                                            Zea diploperennis (Diploperennial teosinte)...
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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EMEL; AY532784; AAT40053.1; ...
EMEL; AY532786; AAT40053.1; ...
EMEL; AY532786; AAT40055.1; ...
EMEL; AY532786; AAT40055.1; ...
EMEL; AY532781; AAT40055.1; ...
EMEL; AY532781; AAT40057.1; AAT40057.1; AAT40057.1; ...
EMEL; AY532781; AAT40057.1; AA
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Probom; PD154900; Glyco_hydro_19; 1.
PROSITE; PS00770; ChtBD1; 1.
PROSITE; PS00774; CHITINASE 19 1; 1.
PROSITE; PS00774; CHITINASE 19 2; 1.
PROSITE; PS00774; CHITINASE 19 2; 1.
PROSITE; PS0941; CHIT_BIND_1_1; 1.
Chitin-binding.
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(TrEMBLrel. 27, I
(TrEMBLrel. 28, I
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4atches 228; Conservative
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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89.7%; Score 1303; DB 2; Length 283;
Best Local Similarity 90.2%; Pred. No. 2.5e-86;
Matches 230; Conservative 8; Mismatches 11; Indels
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                                                                                          (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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OGJBR1;
05-JUL-2004 (TrEMBLrel. 27, Created)
                                  PRT;
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                                        PRELIMINARY;
                                                                                             05-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
Chitinase.
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Q6JBQ4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                       Tillink;

"Comparative evolutionary histories of chitinase genes in the genus

"Comparative evolutionary histories of chitinase genes in the genus

"Comparative stars 1311-134(1204).

"Edenetics 167:1311-134(1204).

"EMBL; AY53722; AAT39991.1; -..

"EMBL; PRO0185; Prittin binding.1; -..

"EMBL; PRO0185; CHITINBINDNG.19; -..

"EMBL; PRO0185; ALDEHYDE DEHYDR GLU; UNKNOWN.1.

"EMBL; PRO0178; PRO0179; ALDEHYDE DEHYDR GLU; UNKNOWN.1.

"EMBL; PRO0179; CHITINASE.19.1; -..

"EMBL; PRO0178; PRO0179; CHITINASE.19.1; -..

"EMBL; PROS178; PRO0179; CHITINASE.19.2; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGSSGG-----SGANVASVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GHFCYISEVNKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRAIGFDGLGDP
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                                                                                         Zea mays (subsp. parviglumis) (Balsas teosinte).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
PACCAD clade, Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7%; Score 1302.5; DB 2; Length 281; 90.2%; Pred. No. 2.7e-86; artive 8; Mismatches 12; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 AA; 28979 MW; C23523FE12D986A6 CRC64;
(TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 24, 2005, 12:54:16
Job time: 118.081 secs
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                                                             Chitinase.
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3

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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May 24, 2005, 12:39:31; Search time 25.3452 Seconds (without alignments) 975.638 Million cell updates/sec Run on:

score:

US-10-692-367-12 1452 1 SMQNCGCQPNVCCSKFGYCG......GYYRQYCRQLGVDPGNNLTC Perfect so Sequence:

257

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

of hits satisfying chosen parameters: Total number

283416 seqs, 96216763 residues

seq length: 0 seq length: 200000000 8 1 1 1 1 1 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chitinase (EC 3.2.			as	chiti	chitinase (BC 3.2.	probable endochiti	a	chitinase class 4	probable chitinase	probable endochiti	chitinase (EC 3.2.	ri	chitinase (BC 3.2.	probable chitinase	chitinase (EC 3.2.		m	probable endochiti	probable endochiti	chitinase (EC 3.2.	probable endochiti	v	chitinase (EC 3.2.	_	chitinase (EC 3.2.	chitinase (EC 3.2.	chitinase (EC 3.2.	chitinase (EC 3.2.
SUMMARIES	ΩI	A42424	B42424	851678	825311	T47601	S46536	A84868	S16579	S57476	T03405	H84867	T14345	T14348	T14344	T14341	T09131	A44039	JE0125	G84867	C84868	S51645	D84868	865778	S05426	T09687	S20981	543317	JC2071	865019
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#	Query Match	91.4	88.6	60.0	59.4	58.3	57.4	56.8	56.2	26.0			54.2	54.1			53.5	52.2		49.3	48.9	48.7	48.1	45.9	44.3	43.8	42.9	٠	42.7	42.6
	Score	1327	1287	870.5	862.5	847	833	824.5	816	812.5	809.5	794	786.5	785.5	777.5	777.5	777.5	757.5	746.5	715.5	710	706.5	698	667	S	o	622.5	621	620	618
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chitinase (EC 3.2.	probable chitinase	chitinase (EC 3.2.	chitinase class 1	chitinase (EC 3.2.											
508627	T03614	865020	S56694	S20982	S37344	S18750	T07838	S38670	T06999	T07000	B45511	T04403	859953	S57482	S15997
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ALIGNMENTS

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C;Species: Zea mays (maize)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-1999
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-1999
C;Datession: A44424; A44226
R;Huynh, O.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.
J. Biol. Chem. 267, 6635-6640, 1992
A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifunga
A;Reference number: A42424; MUID:92202208; PMID:1551872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the catalytic site of a chit
                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A42424
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-280 «HUY>
A;Experimental source: seed
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:89874, NCBIP:89876)
B;Note: sequence extracted from NCBI backbone (NCBIN:89874, NCBIP:89876)
B;Note: Sequence axtracted from NCBI backbone (NCBIN:89874, NCBIP:89876)
A;Note: Sequence axtracted from NCBI backbone (NCBIN:89874, NCBIP:89876)
A;Note: Sequence axtracted from NCBI backbone (NCBIN:89874, NCBIP:89876)
A;Title: Identification of an essential tyrosine residue in the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opyl) - carbodiimide.
A;Reference number: A42260; MUID:92156129; PMID:1740436
A;Accession: A42260
chitinase (EC 3.2.1.14) A - maize
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 180-195 < VER>
A; Nesidues: 180-195 < VER>
A; Note: the residue designated 'X' was determined to be derivatized tyrosine; therefore, C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Keymords: glycosidase; hydrolase; polysaccharide degradation
F; 25-6-61/Domain: hevein chitinase pomology < PCH>
F; 82-280/Domain: plant chitinase homology < PCH>
F; 188/Active site: Tyr #status predicted

ö Gарв ö Score 1327; DB 2; Length 280; Pred. No. 8.88-98; 9; Mismatches 15; Indels Query Match
Best Local Similarity 90.6%;
Matches 231; Conservative

QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANVVT

62

122 145 182 85 QNCGCQPNPCCSKFGYCGTTDAYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANVVT DAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATHET DAFFNGIKNQAGSGCEGKNFYTRSAFLSAVNAYPGFAHGGTEVEGKREJAAFFAHVTHET 56 63 123 요 à ò ద ò

205 GHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDP 146 염. 장

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9 62

Gaps

237

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A; Residues: 1-268 <RAS>
A; Residues: 1-268 (RAS>
A; Residues: 1-268 (RAS>
A; Cross-references: UNIPROT:006209; EMBL:X61488; NID:g17798; PIDN:CAA43708.1; PID:g17799
A; Cross-references: UNIPROT:006209; EMBL:X61488; NID:g17799
C; Superfamily: lectin-related plant chitinase; hevein chitinase degradation
F;1-24/Domain: signal sequence #status predicted <SIG>
F;2-26/Product: chitinase #status predicted <MAT>
F;25-66/Domain: hevein chitin-binding domain homology <HCB>
F;74-268/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brassica napus (rape)
C;Species: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C;Accession: $25311
C;Accession: $25311
F;Rasmussen, U; Bojsen, K.; Collinge, D.B.
Plant Mol. Biol. 20, 277-287, 1992
A;Title: Cloning and characterization of a pathogen-induced chitinase in Brassica napus.
A;Reference number: $25311; MUID:93004480; PMID:1391771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                                                                                                                                                                                                                                                                            ETGHECYISEVN-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGL 179
                                                                                                                                                                                                                                                                                                                                                                                                  GDPGIVARDPVISFRASIWFWMNNCHSRIISGQGFGSTIRAINGNLECNGANPGTVTTRV 241
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                                                                                                                      SMONCGCOPINYCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                           SGONCGCAPNICCSOFGYCGSDAAYCGEGCRSGPCY------GSNPGSASSVANI
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                                                                 15;
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   Length 261;
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DB 2;
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                                                              60;
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      60.0%; Score 870.5; DB 59.6%; Pred. No. 1e-61; ive 30; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chitinase (EC 3.2.1.14) precursor - rape
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                                                                    Conservative
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   Query Match
Best Local Similarity
Matches 155; Conserv
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Best Local
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Cipteriage (EC 3.2.1.14) proper (EC 3.2.1.14) properties (EC 3.2.1.14) proteins (EC 3.2.14) proteins (EC 3.2.14)
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NyAlernate names: pathogenesis-related protein PR-3 type
C;Species: Sambucus nigra (European elder)
C;Date: 07-May-1995 #sequenc_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51678
R;Coupe, S.A.; Taylor, J.E.; Roberts, J.A.
submitted to the EMBL Data Library, December 1994
A;Description: Characterisation of mRNAs that encode pathogenesis-related proteins that
A;Reference number: S51678
A;Accession: S51678
A;Accession: S51678
A;Accession: S51678
A;Accession: S51678
A;Accession: COUP
A;Residues: 1-Zel .cOUP
A;Residues: 1-Zel .cOUP
A;Residues: 1-Zel .cOUP
A;Coose-references: UNIPROT:Q43150; EMBL:Z46948; NID:g603881; PIDN:CAA87072.1; PID:g6038
C;Superfamily: lectin-related plant chitinase; hevein chitinase; hevein chitinase; cyclosidase; polysaccharide degradation
F;16-51/Domain: blant chitinase homology <PCH>
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Best Local Similarity 89.0'
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                  YCROLGVDPGNNLTC
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probable endochitinase [imported] - Arabidopsis thaliana
probable endochitinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Accession: A84668
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
eus, D.; Micrman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Redocule type: DNA
A;Residues: 1-264 <GTO>
A;Cross-references: UNIPROT:024658; GB:AE002093; NID:92281111; PIDN:AAB64047.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: At2g43590
A;Map position: 2
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chitinase (EC 3.2.1.14) precursor - kidney bean C; Species: Phaseolus vulgaris (kidney bean)
C; Species: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C; Accession: S16579
R; Margis-Pinheiro, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.; Burkard Plant Mol. Biol. 17, 243-253, 1991
A;Title: Isolation of a complementary DNA encoding the bean FR4 chitinase: an acidic enz
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                                              78 PGTGGGGSSVSDIVSQAFFDGIIGQAAASCPGKNFYTRAAFLSAVD--PKFGNEGSSDDN 135
                                                                                                                                                            YNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALE 224
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                 -GGGSGGANVANVVTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVER
                                                                                                                               KREIAAFFAHATHETGHFCYISE--VNKSNAYCDPTK-RQWPCAAGQKYYGRGPLQISWN
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                                                                                                                                                                                                                                                                                                                                                                                  256 CNGQNQQANDRIQFYKKYCADFGVAPGDNLTC 288
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S46356
chitinase (EC 3.2.1.14) - beet
C; Species: Beta vulgaris (beet)
C; Species: Beta vulgaris (beet)
C; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C; Accession: $46536
R; Nielsen, K.K.; Bojsen, K.; Roepstorff, P.; Mikkelsen, J.D.
Plant Mol. Biol. 25, 241-257, 1994
A; Title: A hydroxyproline-containing class IV chitinase of sugar beet is glycosylated wing R; Reference number: $46536; MUD: 94289648; PMID: 8018873
A; Rocession: $46536
A; Stetus: preliminary
A; Molecule type: mRNA
A; Residues: 1-288 ANIE>
A; Cross-references: UNIPROT: P42820; EMBL: L25826; NID: 9510277; PIDN: AA322916.1; PID: 95102
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: glycosidase; hydrolase; polyaaccharide degradation
F; 28-64/Domain: plant chitin-binding domain homology <HCB>
F; 89-288/Domain: plant chitinase homology <PCH>
class IV chitinase (CHIV) - Arabidopsis thaliana
N;Alternate names: protein T12E18.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000
R;Baloecker, H.; Newes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,
R;Bloecker, H.; Newes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224469
A;Reference number: 224469
A;Reference number: 224469
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-273 emb.
A;Residues: 1-273 emb.
A;Resperimental source: cultivar Columbia; BAC clone T12E18
C;Genetics:
A;Map posttion: 3
A;Introns: 139/1
A;Note: T12E18.110
C;Superfamily: lectin-related plant chitinase; hevein chittin-binding domain homology; pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 273;
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57.1%; Pred. No. 1e-58;
ive 33; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNCGCQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.3%; Score 847; DB 2; Best Local Similarity 59.4%; Pred. No. 7.8e-60; Matches 152; Conservative 27; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNCGCAPNLCCSNFGFCGTGTPYCGVGNCQSGPCE-
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Best Local Similarity 57.1<sup>3</sup>
Matches 156; Conservative
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Best Local S
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3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGANVANVVT
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           239
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c)Species: Vigna unguiculata (cowpea)
C)Species: Vigna unguiculata (cowpea)
C)Species: Vigna unguiculata (cowpea)
C)Accession: $57476
R;Vo, L.T.T.; Broughton, W.; Krause, A.
A;Reference number: $57468
A;Accession: $57476
A;Accession: Companiation
B;Accession: $57476
A;Cross-reference: UNTRROT:Q43686; EMBL:X88803; NID:g871767; PIDN:CAA61281.1; PID:g8717
A;Cross-reference: UNTRROT:Q43686; EMBL:X88803; NID:g871767; PIDN:CAA61281.1; PID:g8717
B;Accession: Prediation Chitinase homology chicked plant chitinase; hevein chitin-binding domain homology; pl
A;Reference number: $16579; MUID:91322521; PMID:1863776
A;Accession: $16579
A;Aolecule type: mRNA
A;Aolecule type: mRNA
A;Residues: 1-270 <MAR>
A;Residues: 1-270 <MAR>
A;Cross-references: UNIPROT:P27054; EMBL:X57187
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;24-59/Domain: hevein chitin-binding domain homology <HCB>
F;20-270/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                                                                                                                                                                                                                                                                                                                                                                                                                       LGDPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                 22 SAQNCGCAEGLCCSQYGYCGTGEDYCGTGCQQGPCTT-----ASPPPSNNVN-ADI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMONCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
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                                                                                                                                                                                                                       Length 270;
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                                                                                                                                                                                                                                                                   65; Indels
                                                                                                                                                                                                                       Query Match 56.2%; Score 816; DB 2; Best Local Similarity 57.9%; Pred. No. 2.2e-57; Matches 150; Conservative 32; Mismatches 65.
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58.3%; Pred. No. 3.8e-57;
ive 30; Mismatches 65
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Best Local Similarity
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A;Experimental source: cv. Nipponbare
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl:
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;30-229/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                          C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 SGGANVANVVTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI
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C,Superfamily: lectin-related plant chitinase, hevein chitin-binding
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R;Truong, N.; Itoh, Y.
submitted to the EMBL Data Library, April 1997
A;Description: Nucleotide sequence of rice class II chitinase cDNA.
A;Reference number: Z14936
A;Accession: T03405
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-229 <TRU>A;Residues: 1-229 <TRU>A;Residues: 1-229 <TRU>A;Cross-references: UNIPROT:004138; EMBL:AB003194
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                                                                                                                                                                                                                                                                                                probable chitinase (EC 3.2.1.14) IIb - rice
231 YYTEYCROLGVDTGDNLTC
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A; Pathway: polygaccharide degradation
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: glycosidase; hydrolase; polygaccharide degradation
F;21-56/Domain: hevein chitin-binding domain homology <HCB>
F;69-266/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami A; Pathway: polysaccharide degradation C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;23-58/Domain: hevein chitin-binding domain homology <PCHP>
F;71-268/Domain: plant chitin-binding <PCH>
F;71-268/Domain: plant chitinase homology <PCH

F;71-268/Domain: plant chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of N-acetyl-D-glucosamı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDPGRVARDAVVAFKAALWFWMNVVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T14348
R;Kragh, K.; De Vries, S.C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z17995
A;Residues: 1-266 <KRA>
A;Residues: 1-266 <KRA>
A;Residues: UNIPROT:Q96411; EMBL:U52848; NID:g1549334; PID:g1549335
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14344
R;Kragh, K.; De Vies, S.C.
R;Kragh, C, the EMBL Data Library, March 1996
A;Reference number: 217995
            C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-268 <KRA>
A,Cross-references: UNIPROT:096409; EMBL:U52846; NID:g1549330; PID:g1549331
A,Experimental source: strain sg766 trophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ETGHFCYISEVN-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catalyzes the hydrolysis of the beta-1,4-linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.1%; Score 785.5; DB 2; 56.2%; Pred. No. 5.5e-55; tive 33; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T14344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 777.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chitinase (EC 3.2.1.14) EP3-2/H1, class IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNSYCSKPGVAPGDNORC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 YRQYCRQLGVDPGNNLTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.24
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14345
R;Kragh, K:; De Vries, S.C.
R;Kragh, K:; De Vries, S.C.
A;Reference number: 217995
A;Accession: T14345
A;Reference number: 217995
A;Reference number: 217995
A;Reference number: 217995
A;Reference number: 217995
A;Residues: 1-266 -KRAA
A;Residues: 1-266 -RRAA
A;Residues: 1-267 -RRA
                                                                                                                                                                              VTDDPFNGIISQATGDCDGKNFYTRSAFLNALQSYSSFGTSGSADDSKREIAAFFAHATH 130
                                                                                                                                                                                                                                                                                            GHFCYISEVN-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETGHFCYISEVN-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGL 179
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                                                                                                                               DAFFNGIKNOAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATHET
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Best Local Similarity 55.8%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels
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T14348
probable chitinase (EC 3.2.1.14) EP3B/E6, class IV - carrot
ONCDCAPNLCCSQFGYCGTTADYCGSTCQSGPCRVGGPPTGAG-
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179

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probable chitinase (EC 3.2.1.14) EP3-1/H5, class IV - carrot (fragment)
C;Species: Daucus carota (carrot)
C;Accession: T14341
R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; K;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; K;Kragh, K.; Toonen, M.J.; Mollos, M.J.; Mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
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                                                                                                                                                                                                                                                                                          ETCHFCYISEVN-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                 GDPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 SAQNCNCAAGLCCSKYGYCGTTSDYCGEGCQAGPCTNSAPSGGG-----NAVSVADI 72
                                                                                                    1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGANVANV 60
                                                                                                                                                                    21 SAQNCNCAAGLCCSKYGYCGTTSDYCGEGCQAGPCTNSAPSGGG-----NAVSVADI 72
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Best Local Similarity 55.0%; Pred. No. 2.4e-54;
Matches 142; Conservative 35; Mismatches 70; Indels 11; Gaps
                                   Gaps
                                   11;
al Similarity 55.0%; Pred. No. 2.4e-54; 142; Conservative 35; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 YNSYCSKFGVAPGDNQGC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 YRQYCRQLGVDPGNNLTC 257
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Search completed: May 24, 2005, 12:55:12 Job time : 26.3452 secs

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; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
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Sequence 12, Application US/10692367

Publication No. US20050050595A1

GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Movel compositions with chitinase TITLE OF INVENTION: Movel compositions with chitinase CURRENT FILING DATE: 2003-10-22

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/303-03-10-22

PRIOR APPLICATION NUMBER: 10/303-03-14

PRIOR FILING DATE: 2003-03-14

PRIOR FILING DATE: 2003-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR PLING DATE: 2001-12-05

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH DATE: 257
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ORGANISM: Artificial Sequence
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| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp: +
| Cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp: +
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gaps

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100.0%; Score 1452; DB 17; Length 257; 100.0%; Pred. No. 5.2e-112; tive 0; Mismatches 0; Indels 0;

Query Match 100. Best Local Similarity 100. Matches 257; Conservative

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Result

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36, Appl
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US-10-692-367-19

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                                                                                                                                                                                                                                                                                                             GENERAL INCORMATION
GENERAL INCORMATION
APPLICANT: MILIORY MACHINES L.
APPLICANT: SIMMONS, CALT R.
APPLICANT: SIMMONS, CALT R.
APPLICANT: SIMMONS, CALT R.
APPLICANT: SIMMONS, CALT R.
APPLICANT: APADENI, NOVEL COMPOSITIONS WITH ChitINASE
TITLE OF INVENTION: ACTIVITY
FILE OF INVENTION: ACTIVITY
FILE OF INVENTION NUMBER: US/10/692,367
CURRENT APPLICATION NUMBER: US/10/389,432
PRIOR PILING DATE: 2003-10-314
PRIOR PILING DATE: 2003-11-07
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-11-07
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Publication No. US2005005055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Yamons, Carl R.
ATTLE OF INVENTION: Activity
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                                                                                                                                                                                                   US-10-692-367-34
; Sequence 34, Application US/10692367
; Bublication No. US2005005055A1
; GENERAL INFORMATION:
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                                         ORGANISM: Artificial Sequence
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                                               SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
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; OTHER INFORMATION: Variant sequence produced by shuffling techniques US-10-692-367-30
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APPLICANT: Muller, Mathias L.
APPLICANT: Miller, Mathias L.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Novel compositions with chitinase
ITILE OF INVENTION: Activity
FILE REFERENCE: 54916,2000130.
CURRENT FILING DATE: 2003-10-22
FRIOR APPLICATION NUMBER: 10/290,086
FRIOR PILING DATE: 2003-11-06
FRIOR PILING DATE: 2002-11-06
FRIOR APPLICATION NUMBER: 60/337,029
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-692-367-30
; Sequence 30, Application US/10692367
; Publication No. US2005005055A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.8%; Score 1405; DB 17; Length 257; Best Local Similarity 95.3%; Pred. No. 4e-108; Matches 245; Conservative 8; Mismatches 4; Indels 0
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Publication No. US20050050531

Sequence 60, Application US/10692367

Publication No. US20050050531

APPLICANT: Muthias L.

APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: NOVel.compositions with chitinase

TITLE OF INVENTION NUMBER: 10/290,086

PRIOR PILING DATE: 2002-10-10

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-22

NUMBER: OF SEQ ID NOS: 84

SOUTHARE PRESENTED NUMBER: 60420,666

SOUTHARE PRESENTED NUMBER: 60420,666

PRIOR FILING DATE: 2001-10-22

NUMBER: OF SEQ ID NOS: 84
PILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 10/389,432
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2001-11-07
SOFTWARE: PASSEQ FOR WINGOWS VERSION 4.0
SOFTWARE: PASSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 72
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ORGANISM: Artificial Sequence
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LENGTH: 256
TYPE: PRT
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; PERATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-60
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                                                                                                          Query Match 95.2%; Score 1382.5; DB 17; Length 256; Best Local Similarity 94.9%; Pred. No. 2.9e-106; Matches 244; Conservative 5; Mismatches 7; Indels 1;
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APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: activity

FILE OF INVENTION: activity

FILE OF INVENTION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-3-14

PRIOR APPLICATION NUMBER: 10/290,086

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2002-10-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PARESEQ for Windows Version 4.0

LENGTH: 257
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US-10-692-367-46
Sequence 46, Application US/10692367
Publication No. US20050050595A1
GENERAL INFORMATION
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Matches 241; Conservative
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                                                                         DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY 240
ETGHECYISEVNKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRAIGFDGLG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Variant sequence produced by shuffling techniques US-10-692-367-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.8%; Score 1377; DB 17; Length 257; Best Local Similarity 93.4%; Pred. No. 8.2e-106; Matches 240; Conservative 8; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Muller, Mathias L.

APPLICANT: True, Thom

APPLICANT: Yalpani, Nases.

TITLE OF INVENTION: Novel compositions with chitinase

CURRENT FILING DATE: 2003-10-22

PRIOR FILING DATE: 2003-11-66

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2003-10-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FREISEQ for Windows Version 4.0

SEQ ID NO 66

LENGTH: 257
                                                                                                                                                                                                                                                                     US-10-692-367-66; Sequence 66, Application US/10692367; Sequence 66, Application US/2050050595A1; GENERAL INFORMATION:
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                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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RESULT 8 US-10-692-367-62

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121 STGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.6%; Score 1373.5; DB 17; Length 256; Best Local Similarity 94.2%; Pred. No. 1.6e-105; Matches 242; Conservative 8; Mismatches 6; Indels 1;
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Publication No. US20050050595A1

GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Alpani, Nases

TITLE OF INVENTION: activity

FILE REFRENCE: 54916200320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-314

PRIOR PILING DATE: 2003-314

PRIOR PILING DATE: 2003-11-06
                                                                                        GENERAL INFORMATION:
APPLICANT: MILIEY, MATHIAS L.
APPLICANT: MILIEY, MATHIAS L.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Novel compositions with chitinase
ITLE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT APPLICATION NUMBER: 10/389,432
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-022
Sequence 62, Application US/10692367
Publication No. US20050050595A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
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; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-48
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                                                                                                                                                                                                                                                                                                                                                Query Match
94.1%; Score 1366.5; DB 17; Length 256;
Best Local Similarity 94.6%; Pred. No. 6e-105;
Matches 243; Conservative 5; Mismatches 8; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/10692367

Sequence 74, Application US/10692367

Sequence 74, Application No. US2005005051

Sequence No. US2005005051

Sequence No. US2005005051

APPLICANT: Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons Carl R.

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: Activity

FILE REFERENCE: 54916200320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/389,432

PRIOR PILING DATE: 2003-03-14

PRIOR PILING DATE: 2002-11-06

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 84

SOFTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 74
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 256
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ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                             1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRP-GGGGGGGGGGGGGANVASV
                                                                                                                                                                                                                                                                                   181 DPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY
                                      1 SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGANVANV
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6; Indels
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APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Novel compositions with chitinase
TITLE OF INVENTION: activity
FILE REPERBACE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT PILING DATE: 2003-10-22
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PARESEQ for Windows Version 4.0
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92.2%; Pred. No. 1.2e-104;
tive 10; Mismatches 10;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-692-367-64; Sequence 64, Application US/10692367; Publication No. US20050050595A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         RQYCRQLGVDPGNNLTC 257
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ORGANISM: Artificial Sequence
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  238; Conservative
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 DPNRVARDPVLAFKAALWFWMNVHRVMPQGFGATIRAINGALKCGGNNPAQMDARVGYY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 257;
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                                                                                                                                                                                                         GRENEAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Yalpani, Nasser

ITILE OF INVENTION: Activity

FILE REFERENCE: $59162000320

CURRENT APPLICATION NUMBER: 105/10/692,367

CURRENT FILING DATE: 2003-10-22

FRIOR PELLING DATE: 2003-10-22

FRIOR APPLICATION NUMBER: 10/290,086

FRIOR FILING DATE: 2001-03-11-66

FRIOR APPLICATION NUMBER: 60/337,029

FRIOR APPLICATION NUMBER: 60/337,029

FRIOR APPLICATION NUMBER: 60/420,666

FRIOR FILING DATE: 2001-11-07

FRIOR FILING DATE: 2002-10-22

NUMBER OF SEQ ID NOS: 84

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.7%; Score 1361; DB 17;
ilarity 92.2%; Pred. No. 1.7e-104;
Conservative 9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/10692367;
Publication No. US2005005055A1
GENERAL INFORMATION:
APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
                                                                                                                              RESULT 12
US-10-692-367-24
Sequence 24, Application US/10692367
Publication No. US200500505551
; GENERAL INFORMATION:
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                                      241 ROYCROLGVDPGNNLTC 257
                                                           ORGANISM: Artificial Sequence
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Matches 237; Conserv
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US-10-692-367-38
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61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
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Sequence 68, Application US/10692367

Publication No. US200S00595A1

GENERAL INFORMATION:
APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
TITLE OF INVENTION: Novel compositions with chitinase
TITLE OF INVENTION NUMBER: U0/389,432

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR PILING DATE: 2003-10-6

PRIOR PILING DATE: 2003-11-06

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2002-11-06

PRIOR PILING DATE: 2002-10-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0
   compositions with chitinase
TITLE OF INVENTION: Novel compositions with C TITLE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-44
PRIOR FILING DATE: 2003-11-06
PRIOR FILING DATE: 2002-11-06
PRIOR FILING DATE: 2001-11-07
SOFTWARE: FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASISEQ for Windows Version 4.0
SSEQ ID NO 38
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                               1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCR8---GGGGGGGGGGGGAAVASV 57
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                                                                                                                                                                                                                        1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                Gaps
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                                              , OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68
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                                                                                                                                   DB 17; Length 254;
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93.2%; Score 1353.5; DB 17; Length 250;
Best Local Similarity 93.4%; Pred. No. 7e-104;
Matches 240; Conservative 3; Mismatches 7; Indels 7;
                                                                                                                              Query Match 93.4%; Score 1356.5; DB 17; Lengt Best Local Similarity 93.0%; Pred. No. 4e-104; Matches 239; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/10692367

| Bublication No. US20050050531
| General INFORMATION: Mathias L. APPLICANT: Muller, Mathias L. APPLICANT: Muller, Mathias L. APPLICANT: Simmons, Carl R. PILE OF INVENTION: NOVel compositions with chitinase; TILE OF INVENTION: NOVEL COMPAGE: 54916-200320
| CURRENT APPLICATION NUMBER: US/10/692,367
| CURRENT APPLICATION NUMBER: 10/389,432
| PRIOR PILING DATE: 2003-01-14
| PRIOR PILING DATE: 2002-11-06
| PRIOR PILING DATE: 2002-11-07
| PRIOR PILING DATE: 2002-11-07
| PRIOR PILING DATE: 2002-10-02
| NUMBER OF SEQ ID NOS: 84
| SOFTWARE FERENCE FOR Windows Version 4.0
| SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ROYCROLGVDPGNNLTC 257
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ORGANISM: Artificial Sequence
FEATURE:
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Db 54 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHVTH 113

Qy 121 ETGHFCYISEVNKSNAYCDPTKRQWFCAAGQKYYGRGFLQISWNYNYGPAGRAIGFDGLG 180

Db 114 ETGHFCYISEINKSNAYCDPTKRQWFCAAGQKYYGRGFLQISWNYNYGPAGRAIGFDGLG 173

Qy 181 DPGRVARDAVVAFKAALWFWMNNVHRVWPQGFGATIRAINGALECNGNNPAQMNARVGYY 240

Db 174 DPGRVARDAVVAFKAALWFWMNNVHRVWPQGFGATIRAINGALECGGNNFAQMNARVGYY 233

Qy 241 RQYCRQLGVDPGNNLTC 257

Db 234 KQYCRQLGVDPGPNLTC 250

Search completed: May 24, 2005, 13:12:27

Job time: 92.7495 8ecs
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Sequence 1, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 24, Appli
Sequence 115, Appli
Sequence 141, Appli
Sequence 14, Appli
Sequence 20, Appli
Sequence 20, Appli
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Sequence 9, Appli
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| Sequence 2, Application US/09522714
| Sequence 2, Application US/09522714
| Patent No. 6563020
| Patent No. 6563020
| APPLICANT: Simmons, Carl R.
| APPLICANT: Simmons, Marser
| TITLE OF INVENTION: Maize Chitinases and Their Use in TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants FILE REFERRACE: 1100
| TITLE NO INVENTION: Enhancing Disease Resistance in Crop Plants FILE REPLICATION NUMBER: 0S/09/522,714
| CURRENT FILING DATE: 2000-03-10
| EARLIER PILING DATE: 2000-03-10
| SARLIER PILING DATE: 1999-03-24
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: FastSEQ for Windows Version 3.0
                              Sequence 3
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US-09-125-891-4
US-08-475-427-1
US-08-478-165-1
US-08-448-398-3
US-08-148-398-3
US-07-791-931-8
US-07-791-931-10
US-07-791-931-10
US-07-791-931-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-873A-10
US-09-138-91-91
US-08-09-138-91-91
US-08-047-413-9
US-08-047-413-9
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Pred. No. 3.4e-103;
9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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US-09-522-714-22
; Sequence 22, Application US/09522714
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Best Local Similarity 89.8%;
Matches 229; Conservative 9
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US-09-522-714-2
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'GGTZ_6/ptodata1/jaa/5A_COMB.pep:*
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'CGTZ_6/ptodata1/jaa/6A_COMB.pep:*
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133 KSNAYCD-PTKROWPCAAGQKYYGRGPLQISMNYNYGPAGRAIGFDGLGDPGRVARDAVV 191
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Patent No. 6133507
GENERAL INFORMATION:
APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin cDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION WUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
GUNBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Solanum tuberosum
US-07-791-931-5
                                                                                                                                                    251 PG 252
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APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT PILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/125,915
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 183
                                                                                                                                                                                                                                                                                                                                                                                 15;
GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Maize Chitinases and Their Use in TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants FILE REFERENCE: 1100

CURRENT APPLICATION NUMBER: US/09/522,714

CURRENT FILING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/125,915

EARLIER APPLICATION NUMBER: 60/125,915

EARLIER PILING DATE: 199-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0
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59.3%; Score 861.5; DB 4.
Best Local Similarity 60.1%; Pred. No. 5.7e-66;
Matches 155; Conservative 30; Mismatches 58.
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254 YKQPCQDPGVDPGNNLTC 271
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ORGANISM: Zea mays
US-09-522-714-30
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ORGANISM: Zea mays
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LENGTH: 271
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEPENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: LOS ANGeles
CITY: LOS ANGeles
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 QNCGSQGGGKACASGQCCSKFGWCGNTNDYCG----SGNCQSQCPGGGPGPGFGGDLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 NVANVVTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QNCG-----CQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 ADRAANRLPGFGVITNIINGGLECGRGTDNRVQDRIGFYRRYCSILGVTPGDNLDC 313
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44.3%; Score 643; DB 3; Length 328;
Best Local Similarity 44.3%; Pred. No. 3.3e-47;
Matches 131; Conservative 36; Mismatches 79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHATHET ------GHFCYISEVNKSNAYCDPTKROWPCAAGOKYYGRGPLOIS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 WNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM-----PQ- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 HNYNYGPCGRAIAVDLLANNPDLVATDPVISFKTALWFWMTPQSPKPSCHDVIIGRWNPSS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 QNCGSQGGGKACASGQCCSKFGWCGNTNDYCG----SGNCQSQCPGGGGPGPGPGGGLGSA 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 -----GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.9%; Score 637; DB 1; Length 33
43.9%; Pred. No. 1.1e-46;
tive 36; Mismatches 80; Indels
ZIP: 90071-2921

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPTRE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FLING DATE: 22-MAY-1991
CLASSITCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,192
RESTERNICE/DOCKET NUMBER: P31,899
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1546-4737
TELERRAK: (619) 546-4332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: ADDRESS:
ADDRESSER: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08379259
Patent No. 5695939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071-2921
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 330 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.98
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE 111
US-07-704-288C-8
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US-08-475-427-13
i Sequence 13. Application US/08475427
i Sequence 13. Application US/08475427
i Patent No. 5859340
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: DEGINAL, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AHATHET-----GHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQIS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 NVANVVIDAFFNGIKNQAGSGCEGKNFYIRSAFLEAIAAYPGFAHGGSEVERKREIAAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 637; DB 1; Length 330;
43.9%; Pred. No. 1.1e-46;
tive 36; Mismatches 80; Indels
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3000 K Street, N.W., Suite 500
                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERNEK/ECOCKET NUMBER: P31 8899
TELECOMMUNICATION:
TELEPHONE: (619) 546-4737
TELEPHONE: (619) 546-9392
                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.9%
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3000 K Street,
CITY: Washington, D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-379-259-8
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55 ANVANVVTDAFFNG-IKNQAGSGCEGK-NFYTRSAFLEAIAAYPGFAHGGSEVERKREIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AFFAHATHET-----GHF----CYISEVNKSNAYCDPTKROWPCAAGOKYYGRGPL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 QISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWWN-----NVHRVM---- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 PQ-----GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 QNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQS-QCPGGGGPGPVTGGDLGS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEPENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                    COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTONSEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Plower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 43.1%; Score 626.5; DB 2; Best Local Similarity 44.1%; Pred. No. 8.5e-46; Matches 132; Conservative 38; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/07704288C; Patent No. 5399680; GENERAL INFORMATION:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 329 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 444 South Flowe
CITY: Los Angeles
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
       VIRGINIA
                                                     22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-704-288C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
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TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 ANVANVVTDAFFNG-IKNQAGSGCEGK-NFYTRSAFLEAIAAYPGFAHGGSEVERKREIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AFFAHATHET-----GHF----CYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM---- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 QISHNYNYGPCGRAIGVDLIANNPDLVATDPVISFKTAIWFWMTPQSPKPSCHDVIIGRWN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 QNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQS-QCPGGGGPGPPVTGGDLGS-- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQ------GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.1%; Score 626.5; DB 2; Length 329;
44.1%; Pred. No. 8.5e-46;
tive 38; Mismatches 76; Indels 53
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION NUMBER: W 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION NUMBER: W 0PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION NUMBER: R 90 09460
ATFORNEY/AGENT INPORMATION:
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELEROMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFORM: (202)672-5309
TELEFRAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/07842165
Patent No. 5932698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRISON, Rene
PRDLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 329 amino acids
amino acid
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APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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US-07-842-165-13
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GENERAL INFORMATION:
APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin cDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SED ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
FILING DATE:
CLASTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relear, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: P31 8899
TELEPHONE: (619) 546-4737
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/07791931C; Patent No. 6133507
                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-07-791-931-6
                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-379-259-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AAFFAHATHET-
                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS: un)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GGGDLGSIISSSMPDQMLKHRNDNACQGKGFYSYNAFINAARSPPGFGTSGDTTARKREI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AAPPAQTSHETTGGWATAPDGPYAWGYCWLREQGSPGDYCTPS-GQWPCAPGRKYPGRGP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM---- 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGFCRSGGGGGGGGGGGGGS 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%; Score 623; DB 1; Length 31(41.5%; Pred. No. 1.6e-45; tive 44; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-379-259-6
; Sequence 6, Application US/08379259
; Batent No. 5655339
; GENERAL INFORMATION:
    APPLICANT: LAMB, CHRISTOPHER J.
    APPLICANT: LAMB, CHRISTOPHER J.
    TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
    TITLE OF INVENTION: DEFENSE REGULATORY
    TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
    ADDRESSE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
    STREET: 444 South Flower Street, Suite 2000
    CITY: LOS Angeles
    STARE: California
    CONFTY: United States
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: Ploppy disk
    COMPUTER: PLOPPY disk
    COMPUTER: PLOPPY DATA:
    APPLICATION NUMBER: US/08/379,259
    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reliev. Stephen B.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECHONE: (619) 546-4737
TELECHONE: (619) 546-9392
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 310 amino acids TYPE: amino acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 41.5*
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-6
      OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 PSSADRAANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDC 295
                                                                                                                                                                        9 SAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGGGG
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                                                              54; Gaps
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Length 310;
                                                        77; Indels
Query Match
42.9%; Score 623; DB 1;
Best Local Similarity 41.5%; Pred. No. 1.6e-45;
Matches 124; Conservative 44; Mismatches 77;
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112 AAFFAHATHET-----GHPCYISEVNKSNAYCDPTKROWPCAAGQKYYGRGP 158
                                                                                                                                                                                                                                                                                                                                                                                            250 QPSSADRAANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDC 309
                                                                                                53 GCANVANVVTDAFFNG-IKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111
                                                                                                                                                                                                                              131 AAFPAQTSHETTGGWATAPDGPYAWGYCWLREQCSPGDYCTPS-GQWPCAPGRKYFGRGP 189
                                                                                                                                                                                                                                                                              159 LQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMNN-------VHRV 207
                                                                                                                                                                                                                                                                                                                                                                208 MPQ------GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
                                                22 ŚAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 70
             APPLICANT: Melchers, Leo S.
APPLICANT: Weulenhoff, Elisabeth J.S.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Moloshuk, Charles P.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,050
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURSHIGS, Kate H.
NAME: MURSHIGS, Kate H.
NAME: MURSHIGS, Kate H.
TELESTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20022.00
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08229050; Patent No. 6066491; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Morrison & Foerster 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 324 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
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TELEX: 706141
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                                                                                                                           117 AAPFAQTSHETTGGWATAPDGPYAWGYCWLREQGSPGDYCTPS-GOWPCAPGRKYFGRGP 175
                                                                                                                                                                                                                                                              208 MPQ------GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
                                                                                                                                                                                                                                                                                  GGANVANVVTDAFFNG-IKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111
                                                                                                                                                                         LQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMNN--------VHRV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICING APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornelissen, Bernardus J.C.
Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
Bol, John F.
Linthorst, Hubertus J.M.
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19-APR-1993
N: acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08047413
Patent No. 5670706
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 324 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.03
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / MOLECULE TYPE: protein US-08-047-413-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 755 Page N
CITY: Palo Alto
STATE: California
                                                                                       112 AAFFAHATHET
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-08-047-413-11
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TELEPHONE:
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US-08-801-563-11
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US-07-704-288C-7
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                                                                                                                                                                                                                                                                                                                                                               LQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALMFWMNN-------VHRV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                208 MPQ------GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
                                                                                                                    1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGG
                                                                                                                                           22 SAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC------PGGPTPP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                Gaps
                                                                                55;
                                        DB 3; Length 324;
                                      42.7%; Score 619.5; DB 3; Length 3
41.0%; Pred. No. 3.3e-45;
tive 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018

ROMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPTICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08801563
Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Mellennoff, Elisabeth J.S.
APPLICANT: Mellennoff, Elisabeth J.S.
APPLICANT: Sela-Buurlage, Mariame B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/801,563
                                 Query Match
Best Local Similarity 41.0%
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-801-563-11
US-08-229-050-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: E
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53 GGANVANVVTDAFFNG-IKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 AAFFAHATHET-----GHFCYISEVNKSNAYCDFTKRQWPCAAGQKYYGRGP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 QPSSADRAANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 LQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKAALWFWMNN-------VHRV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 MPQ------GFGATIRAINGALECNGNNPAQMNARVGYYRQYCRQLGVDPGNNLTC 257
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                                                                                                                                                                                                                                                                                                                                                          22 SAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC------PGGPTPP 70
                                                                                                                                                                                                                                                                                                                                1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGG
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Bacterian Information:
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET 44 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                          Query Match 42.7%; Score 619.5; DB 3; Length 324; Best Local Similarity 41.0%; Pred. No. 3.3e-45; Matches 123; Conservative 43; Mismatches 79; Indels 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen B.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 931,8899
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                            LENGTH: 324 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 90071-2921
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
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| TOPOLOGY: unknown | Colored | Colo
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Search completed: May 24, 2005, 12:56:20 Job time : 33.428 secs

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24, 2005, 12:19:56; Search time 117.095 Seconds (without alignments)
848.864 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 protein search, using sw model
                                                                                                                     May
                                                                                 •
                                                                               OM protein
                                                                                                                       Run on:
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1452 1 SMQNCGCQPNVCCSKFGYCG......GYYRQYCRQLGVDPGNNLTC 257 US-10-692-367-12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneedp19908: * geneedp20008: * geneedp20028: * geneedp20028: * geneedp20038: * geneedp20038: * A_Geneseq_16Dec04:* .: geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

,		عد			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	DB	ID	Description	
				1			:
-	1452	100.0	257	œ	ADS92628	_	3'Be
7	1435	98.8	257	8	ADS92646	_	яве
m	1435	98.8	257	80	ADS92650	_	зве
4	1405	96.8	257	æ	ADS92688	Ads92688 Chitinase	ase
S	1382.5	95.2	256	œ	ADS92676	Ads92676 Chitinase	зве
9	1382	95.2	257	æ	ADS92662	Ads92662 Chitinase	3.Be
7	1377	94.8	257	œ	ADS92682	Ads92682 Chitinase	зве
œ	1373.5	94.6	256	æ	ADS92678	_	38e
6	1366.5	94.1	256	æ	ADS92664	Ads92664 Chitinase	38e
10	1365.5	94.0	256	æ	ADS92690	Ads92690 Chitinase	38e
11	1363	93.9	257	œ	ADS92680	Ads92680 Chitinase	ase
12	1361	93.7	257	80	ADS92654	_	ase
13	1361	93.7	257	ထ	ADS92640	_	38e
14	1356.5	93.4	254	8	ADS92684	Ads92684 Chitinase	38e
15	1353.5	93.2	250	æ	ADS92660	_	зве
16	1351.5	93.1	256	æ	ADS92700	Ads92700 Chitinase	ase
17	1342	92.4	259	æ	ADS92656	_	38e
18	1339	92.2	259	œ	ADS92692	_	38e
19	1338.5	92.2	250		ADS92698	Ads92698 Chitinase	зве
20	1333.5	91.8	254		ADS92642	Ads92642 Chitinase	38e
21	1333	91.8	255		ADS92617	Ads92617 Maize	chi
22	1332	91.7	257		ADS92624	Ads92624 Chitinase	ase
23	1327	91.4	280		ADS92635	Ads92635 Maize	chi
24	1323.5	91.2	250	œ	ADS92668	Ads92668 Chitinase	зве
25	1320	90.9	280	80	ADS92633	Ads92633 Maize	chi

86 Chitinase	8	~	N	94 Chitinase	Ö	_	Chitin	18 Maize chi	94 A maize c	66 Chitinase	_	38 Chitinase	48 Chitinase	_	70 Chitinase	~	44 Chitinase	30 Chitinase	22 Chitinase
Ad892686	Ad89265	Ad89265:	Ad89263	Ad89269	Ad89267	Ad89262	Ads92696	Ads9261	Aab18894	Ad892666	Ads92674	Ads92638	Ads92648	Ads92634	Ad89267	Ads92636	Ads92644	Ad89263	Ads9262:
ADS92686	ADS92658	ADS92652	ADS92632	ADS92694	ADS92672	ADS92620	ADS92696	ADS92618	AAB18894	ADS92666	ADS92674	ADS92638	ADS92648	ADS92634	ADS92670	ADS92636	ADS92644	ADS92630	ADS92622
œ	æ	æ	æ	æ	œ	œ	œ	æ	m	6 0	œ	œ	æ	æ	œ	œ	8	æ	80
250	256	250	258	250	250	258	249	248	281	250	250	250	250	269	250	270	250	251	251
90.8	8.06	90.6	90.6	89.9	89.8	9.68	89.5	89.4	89.4	89.2	89.5	89.0	88.9	98.6	88.3	87.8	87.7	84.0	83.9
1318.5	1318.5	1315.5	1315.5	1305.5	1304.5	1300.5	1299	1297.5	1297.5	1295.5	1294.5	1292.5	1290.5	1287	1282.5	1275.5	1273.5	1220	1218
26	27	28	29		31		33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera. New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode. Yalpani N; ADS92628 standard; protein; 257 AA True I, Simmons CR, Chitinase variant polypeptide #5. (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC. 22-OCT-2002; 2002US-0420666P. 06-NOV-2002; 2002US-00290086. 14-MAR-2003; 2003US-00389432. 22-OCT-2003; 2003WO-US033588 02-DEC-2004 (first entry) WPI; 2004-365417/34. N-PSDB; ADS92627. WO2004037194-A2 06-MAY-2004. Muller ML, Synthetic. ADS92628; ADS92628

The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention. Claim 26; SEQ ID NO 12; 197pp; English

Sequence 257 AA;

Sequence 257 AA;

us-10-692-367-12.rag

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                                                                                                                                          VIDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGPAHGGSEVERKREIAAFFAHATH 120
                                                                                                                                                                                                       ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180
                                                                                                                                                                                                                                           DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY 240
                                                                                                                     VTDAPFNGIKNOAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                                                                                                                                                                                  ETGHPCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                           SMONCGCOPINYCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGGANVANV
                                                                             1 SMONGGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGGANVANV
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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Length 257;
                            0; Indels
100.0%; Score 1452; DB 8;
100.0%; Pred. No. 4.5e-123;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 30; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADS92646 standard; protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitinase variant polypeptide #12.
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(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                            ROYCROLGVDPGNNLTC 257
                                                                                                                                                                                                                                                                                                                                         ROYCROLGVDPGNNLTC 257
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2003; 2003WO-US033588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                              257; Conservative
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N-PSDB; ADS92645.
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                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004037194-A2.
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 Query Match
Best Local
                                Matches
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180
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                                                                                                            VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                                                                                                                              ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180
                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                      9
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                                                                      1 SMONGGCQPINVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                  181 DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY
                                                     1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGGANVANV
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chitinase polynuclectides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                            ö
  Length 257;
                            Indels
 Score 1435; DB 8;
Pred. No. 1.5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yalpani N;
                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 34; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                             ADS92650 standard; protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitinase variant polypeptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             True T, Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                241 ROYCROLGVDPGNNLTC 257
98.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2003; 2003WO-US033588
                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2004 (first entry)
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-365417/34.
               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004037194-A2
                            254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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  Query Match
                 Local
                              Matches
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chitinase variant polypeptide of the invention.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                   96.8%;
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                                                                                                    Best Local Similarity 95.3
Matches 245; Conservative
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                                            Sequence 257 AA;
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                                                                                   Query Match
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ID ADS9

AC ADS9

XX ADS9

XX ADS9

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                                                                                                                                                                                                                                                                                                                                                                                    DPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY 240
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                                                                                                                                                                                                                                                                                                                                                                                                             1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                              1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                                                    61 VIDAFFNGIKNOAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH
                                                                                                    Gaps
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                                                                                                    ö
                                                             Length 257;
                                                                                                    Indels
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                                                           Score 1435; DB 8;
Pred. No. 1.5e-121;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS92688 standard; protein; 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitinase variant polypeptide #33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROYCROLGVDPGNNLTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                           98.8%;
98.8%;
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                                                     Query Match 98.81
Best Local Similarity 98.83
Matches 254; Conservative
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                   Sequence 257 AA;
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                                                                                                                                                                                                                                                                                61 VTDAFFNGIKSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATH
                                                                                                                                                                                                                                                                                                                                                                                               DPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY
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                                                                                                                                                                                 1 SMONCGCOPNVCCSKFGYCGTTDBYCGDGCOSGPCRSGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                                                                             VTDAPFNGI KNQAGSGCEGKNFYTRSAFLEA I AAY PGFAHGGSEVERKREI AA PPAHATH
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                                                                                                                           SMONCGCOPIVCCSKFGYCGTTDBYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGANVANV
                                                               Gaps
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   Length 257;
                                                            4; Indels
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8
Score 1405; DB 8.
Pred. No. 8e-119;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS92676 standard; protein; 256
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(PION-) PIONEER HI-BRED INT INC
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Claim 3; SEQ ID NO 66; 197pp; English.
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                                                                                                                                                                                                                                                                                                                                                ADS92682 standard; protein; 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                       241 ROYCROLGVDPGNNLTC 257
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                       Best Local Similarity 93.8
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADS92681.
                                        Sequence 257 AA;
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                                                                                                                                               DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAOMNARVGYY 240
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                                                                                                         1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANV
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chitinase polynucleotides and polypeptides, useful in producing
plants with enhanced resistance against a fungus or a nematode.
plant resistance to a fungus or nematode. This sequence represents chitinase variant polypeptide of the invention.
                                                                      1,
                                                    Length 256;
                                                                        7; Indels
                                                 Score 1382.5; DB 8;
Pred. No. 8.7e-117;
5; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 46; 197pp; English.
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                   95.2%;
94.9%;
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                                                                        Matches 244; Conservative
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                                                   Query Match
Best Local Similarity
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                               Sequence 256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
Heterodera. The polynuclectides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                            VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH
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                                                                                                                                                                                                                                                                                            1 SMONGCOPHVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGGANVANV
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                                                                                                                                                                                 Length 257;
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                                                                                                                                                                           95.2%; Score 1382; DB 8;
93.8%; Pred. No. 9.7e-117;
live 9; Mismatches 7;
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Chitinase; plant
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                                                            Sequence 256 AA
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                                                                                                                                                                                                         ETGHFCYISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLA 180
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            enhancing
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                                                                                                          SMONCGCOPINVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGGGANVANV
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in producing or a nematode.
 fungus is from the genus Pusarium. The nematode is from the genus theteroderar. The polynuclectides and polynpeptides are useful in enha plant resistance to a fungus or nematode. This sequence represents chitinase variant polypeptide of the invention.
                                                                                       ö
                                                                    Length 257;
                                                                                       Indels
                                                                   Score 1377; DB 8;
Pred. No. 2.8e-116;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chitinase polynucleotides and polypeptides, uplants with enhanced resistance against a fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yalpani N;
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fungus is from the genus Fusarium.
Heterodera. The polynucleotides and
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                                                                                                                                                                                                                                                                                                                                                                                              Chitinase variant polypeptide #28
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                                                                                                                                                                                                                                                                                                                                     ADS92678 standard; protein; 256
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2002US-00290086.
2003US-00389432.
                                                                    94.8%;
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                       Conservative
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                                                                             Similarity
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06-NOV-2002; 2
14-MAR-2003; 2
                                                                 Query Match
Best Local Simil
Matches 240; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2003;
                                                  Sequence 257
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polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heteroderar. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VIGSFFWGIKSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 DPGKVARDAVVAFKAALWFWANNVHRVMPQGFGATIRAINGALECDGNNPAQMNARVGYY
                                                                                                                                                                                                                                                                                                                                                  1 SMONCGCOPNVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY
                                                                                                                                                                                                                                                                                                                                                                                                        1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRP-GGGGGGGGGGGGGGGGGANVASV
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                                                                                                                                                                                                                                8; Length 256;
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                                                                                                                                                                                                                          Score 1373.5; DB 8;
Pred. No. 5.7e-116;
8; Mismatches 6;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 94.2
Matches 242; Conservative
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                                                                                                                                                                                                                                                    VTDAPFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                                                                                                                                                                                                                      ETGHFRYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 179
cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is a from the genue Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or
                                                                                                                                     SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGGGGGGGGGGGGGGANVASV
                                                                                                                           1 SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
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                                                                                      DB 8; Length 256;
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                                                                                     94.1%; Score 1366.5; DB 8 94.6%; Pred. No. 2.4e-115; ive 5; Mismatches 8;
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(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                ADS92690 standard; protein; 256
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2003US-00389432
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                                                                                               sal Similarity 94.6
243; Conservative
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N-PSDB; ADS92689
                                                                    Sequence 256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Fusarium. The nematode is from the genus heteroderar. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                    ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG
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                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                         94.0%; Score 1365.5; DB 8; 92.6%; Pred. No. 3e-115; ive 12; Mismatches 6;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                      Sequence 256 AA
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nes 238;
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                                                                                                                                                                                                                                                                                                                             ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180
                                                                                                                                                                                                                                                                                                                                              ETGHFCYISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQLSWNYNYGPAGRDIGFNGLA 180
                                                                                                                                                                                                                                                                                                                                                                                      DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYY 240
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           nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Pusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                             SMONCGCOPNFCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGANVANV
                                                                                                                                                                                                             SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANV
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encoding them. A method of enhancing plant resistance to a fungus
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                                                                                                                                                       Length 257;
                                                                                                                                                                               10; Indels
                                                                                                                                                     ; Score 1363; DB 8;
; Pred. No. 5.1e-115;
10; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS92654 standard; protein; 257 AA
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                                                                                                                                                       93.9%;
92.2%;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                  Query Match
Best Local Similarity 92.2'
Matches 237; Conservative
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                                                                                                                          Sequence 257 AA;
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                                                                                   enhancing
The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                                                                                                                                                                                                           BIGHFCY1SEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFNGLA
                                                                                                                                                                                                                                                                                                                                                                                                        DPNRVAQDAVVAFKAALWFWMNSVHGVVPQGFGATTRAINGALECNGNNPAQMNARVGYY
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                                                                                                                                                                                                                                                                              VTDAFFNG1KNQAGSGCEGKNFYTRSAFLEA1AAYPGFAHGGSEVERKRE1AAFFAHATH
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                                                                                                                                                                   DB 8; Length 257;
                                                                                                                                                                                             Indels
                                                                                                                                                                                             11;
                                                                                                                                                               Score 1361; DB 8;
Pred. No. 7.7e-115;
8; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitinase variant polypeptide #9.
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(PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                  93.78;
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14-MAR-2003; 2003US-00389432.
                                                                                                                                                                               Best Local Similarity 92.6
Matches 238; Conservative
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                                                                                                                                           Sequence 257 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 DPDRLAQDPVLSFKSALWFWMNVHRVMPQGFGATIRAINGALECGGNNPAQMNARVGYY 240
       The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                        Score 1361; DB 8; Length 257;
Pred. No. 7.7e-115;
9; Mismatches 11; Indels (
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                                                                                                                                                                                                           Local Similarity 92.2
nes 237; Conservative
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                                                                                                                                                              Sequence 257 AA;
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                                                                                                                                                                                                                                                                                                     VTDAFFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
                    The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                      Score 1356.5; DB 8; Length 254;
Pred. No. 1.9e-114;
9; Mismatches 6; Indels 3;
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Claim 3; SEQ ID NO 68; 197pp; English.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 93.0°
Matches 239, Conservative
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                                                                                                                                                                 Sequence 254 AA;
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The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The Hungus is from the genue Pusarium. The nematode is from the genue Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                     Claim 3; SEQ ID NO 44; 197pp; English.
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Sequence 250 AA;

ï 61 VTDAPFNGIKNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAFFAHATH 120 54 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFPAHTH 113 ETGHFCYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180 ETGHFCYISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 173 1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGANVANV 60 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGG-----GGANVANV 53 7; Gaps Query Match
93.2%; Score 1353.5; DB 8; Length 250;
Best Local Similarity 93.4%; Pred. No. 3.6e-114;
Matches 240; Conservative 3; Mismatches 7; Indels 7; 114 121 ઠ g ઠે 중 음 a ò

Search completed: May 24, 2005, 12:50:19 Job time : 118.095 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result		Query				٠	
No.	Score	Match	Match Length DB	图	di 	Description	no
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73	9.209	78.5	928	4	BG837479	BG837479	Zm10 10h0
о Э	597.6	77.2	855	4	BG837663	BG837663	Zm10_01e1
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80	525.6	67.9	628	4	BM736454	BM736454	9520 <u>5</u> 1 <u>A</u> 06
σ	519.4	67.1	837	7	CN133023	CN133023	OX1 9 D11
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DB 3; Length 1179;

89.4%; Score 691.8;

Query Match

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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morrhing (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."
                                                                                                                                                                                                                                                                                          /clone="zml0_10h09"
/tissue type="61hk"
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Hours After Silk
                                                Contact: Harris, Linda J.

Bastern Cereal and Oilseed Research Centre
Bastern Cereal and Oilseed Research Centre
Budy. 21, Central Experimental Farm, Ottawa, Ontario, KIA (CANADA
Tel: (613) 759-1314
Fax: (613) 759-5566
Email: harrisljaggr.gc.ca.
Email: Location/Qualifiers
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Pred. No. 1.3e-113;
6; Mismatches 61; Indels 11
Expressed Sequence Tags from Maize Silk Six Ho
Channel Inoculation with Fusarium graminearum
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/cultivar="CO388"
/db_xref="taxon:4577"
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Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A, Sprott, D. and Tinker, N.A.
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                                                                                                                                               CGACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAACTT
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                                                       GCAGAACTGCGGCTGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC
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                       47; Indels
       Pred. No. 9.8e-131;
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        93.9%;
                          720; Conservative
        Similarity
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Zea mays
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CO524416
3530 1 161 1 E12.y 1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays CDNA, mRNA sequence.
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                                                      577 ATCGCCCCTTCTTCGCGCACGCCACGCACGAGACCGGGCATTTCTGCTACATCAGCGAG
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                                                                                                   151 GGCAGTGGCGGTGCGAACGTGGCTAATGTGGGTCACGACGCGTTCTTCAACGGCATCAAG
                                                                                                                                  756 GGGGGGGGGGGGGGAACGTGGCTAGCGTCATCACGGCTCCTTCTTCAACGGCATCAAG
                                                                                                                                                                                                                                    271 GCCATCGCCGCGTACCCGGGCTTCGCGCATGGCGGCTCCGAGGTCGAGCGCAAGCGCGAG
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                                  CAGAAGTACTACGGGCGCGGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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/organism="Zea mays"
/organism="Zea mays"
/olltivar="COB8"
/db_xref="taxon:4577"
/clone="Zm.0 01e10"
/tissue_type="Sllk"
/dev_stage="4-5 days post-silk emergence"
/clone_lib="Zm.0_AAFC_ECORC_Fusarium_graminearum_corn_silk
                                                                                                                                                                                                                                                                                                 ZM10_01e10_A ZM10_AAFC_ECORC_FUSArium_graminearum_corn_silk_Zeamays_cDNA_clone_Zm10_01e10, mRNA_sequence.
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1 (bases 1 to 855)
1 (bases 1 to 855)
1 Androis, Androis, Saparno, A., Couroux, P., De Moors, A., Hattori, J. I., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D. and Tinker, N.A.

Sprott, D. and Tinker, N.A.

Channel Inoculation with Fusarium graminearum
Unpublished (2001)
 604
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                                                                                  621 ACAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCG
                           561 CCAACAGGGGGGGGGGGCGGGGATCGCGTTCAAGACGGCGCTCTGGTTCTGGATGA
                                                                ACAACGTGCACCGTGTGATGCCGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCG
                                                                                                                               GTATGCTGCAGCAAGTTTGGCTACTGCGGCACCGACGACGAGTACTGCGGCGGCGGCGGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Harris, Linda J.
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 23;
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                                                                                                                                                                                                 725 AGTACTGCCGCCAGCTCGGCGTCGACCCGGGCAACAACC 763
                                                                                                                                                                                                                   741 AGTACTGCCAGCCMCTCCGCGTCSACCCAGGGGCCCAMC 779
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Pred. No. 1.5e-111;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualifiers
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Best Local Similarity 90.3
Matches 670; Conservative
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Suranya, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukarnya; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade, Panicodeae; Andropogoneae; Zea.

1 (Dases 1 to 737)

1 (Dases 1 to 737)

2 Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F., Larkins,B., Becraft,P. and Messing,J.

1 Characterization of the maize endosperm transcriptome and its comparison to the rice genome

2 Genome Res. 14 (10), 1932-1937 (2004)

3 Contact: Lai, Jinsheng

4 Contact: Lai, Jinshery 1937

5 Contact: Lai, Jinshery 1937

6 Contact: Lai, Jinshery 1937

7 Serlinghyusen Rd., Piscataway, NJ 08854, USA
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EL01N0364B04.b Endosperm_3 Zea mays cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Endosperm of 7-23DAP"
/clone lib="Endosperm 3"
/note="Vector: pBluesCript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                    546 CGGCAGGCIGGCGCGCGCGCCGTGGTGCGTTCAAGGCGGCGCCTCTGGTTCTGGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jlai@waksman.rutgers.edu
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/mol_type="mRNA"
/cultivar="W22"
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|lab_host="DH108"
|clone_lib="3530 - Full length cDNA library created by
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        Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530 1 161 1 row: E column: 12.
LocaTion/Qualifiers
                                                                                                                                                                                                                                                                       tissue_type="multiple"
                                                                                                                                                                                                                                            db xref="taxon:4577"
                                                                                                                                                             organism="Zea mays"
'mol_type="mRNA"
'cultivar="B73"
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Inbrary was prepared by George Rudenko using poly (A) library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400mp) and non-directionally cloned into EcoRI-dispersed pulcil y ector. Blue/white selection on carbenicillin-containing plates was used to recover
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/clone_llb="952 - BMS tissue from Walbot Lab (reduced
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                                /mol_type="mRNA" (Black Mexican Sweet)" /cultivar="BMS (Black Mexican Sweet)" /db_xref="taxon:4577" /tisue_type="suspension culture" /dev_stage="mixed_logarithmic and statphases"
                                                                                                                                                                                                                                                                                                                                                                                                Score 530.4; DB 5;
Pred. No. 7e-98;
0; Mismatches 46;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 positive clones."
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Best Local Similarity 92.4%;
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                                                                                                                     GAGGCAGTGCCGCGCGCGGGCCAGAAGTACTACGGGCCGCGCCCCCTGCTAGAATCTC
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                                CGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCCGTGCCGCTCGGGCGGCGGTGGCGG
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Department of Biological Sciences
Branford University
BSS California Ave, Palo Alto, CA 9.
Tel: 650 723 2227
Fax: 650 725 8221
Fax: 670 725 8221
Fax: 670 725 8221
Fax: 720 725 8221
Fax: 720 728 7221
Fax: 720 728 7221
Fax: 720 728 7201
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                     Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                      Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                     column: 10
                                                                                                                                                                                                                                                                              'tissue type="multiple"
dev stage="varies by tissue"
lab_host="DH108"
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/mol_type="mRNA"
/cultivar="B73"
                                                                                                                                                                                                                   Plate: 3530 1 132 1 row: F Location/Qualifiers
                                                    CO520138.1 GI:50325012
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 RESULT 7
CO520138
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FEATURES

COMMENT

DB 7; Length 716;

Score 529.2; DB 7 Pred. No. 1.2e-97;

68.4%; 93.5%;

Query Match Best Local Similarity

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628 bp mRNA linear EST 01-MAR-2002
952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
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65
                                                                                                  236 CGGCGGCGGCGGCGGCGGCGGCGGCGCGCGCGCGGAGCGTGCCAATGTGTGCTAC
                                                                                                                                                                                                                                                                                                                                        296 CGACGCGTTCTTCAACGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAACATT
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Department of Biological Sciences
Stanford University
Tal: 650 723 2227
Fax: 650 725 8221
Fax: 650 725 8221
Plate: 952051 row: A column: 06.
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/Ultivar="BTX623"
/Gultivar="BTX623"
/Gultivar="BTX623"
/Gb_ref="Laxon:4558"
/Glone="OX1 9 Dil A002"
/Glone="OX1 9 Dil A002"
/Glone="OX1 9 Dil A002"
/Glone="Dil BB-T] phage-resistant B. coli"
/Glone="Drain: Leaf and Root; Vector: pRE185-FL3; Site 1:
/Roof; Site 2: Xho1; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.03% and leaves
were misted with 10 um methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
undirectionally into different DrailI site is GACTGTGG,
3-prime DrailI site is CACCATGTG). XhoI excises the cDNA
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 837)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots Other EST9: OX1 9 D11.b1 A002
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmprattworder.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                 01-APR-2004
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OXI_9_D11.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor CDNA clone OXI_9_D11_A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
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Sorghum bicolor
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706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                    Intrary was prepared by George Rudenko using poly (A) elected RNA and Universal Ribochone CDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo (dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >4000pb) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                          /tisaue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
phases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 525.6; DB 4; Length (Pred. No. 6.7e-97; O; Mismatches 49; Indels
                                                                                             mol_type="mRNA"
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'db_xref="taxon:4577"
                                                                 organism="Zea mays"
.ocation/Qualifiers
                                                                                                                                                                                                                                                                                              /lab host="DH10B"
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Best Local Similarity 91.9%;
Matches 566; Conservative (
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647 organism="Saccharum officinarum" mol_type="mRNA" dob_type="mRNA" clone="SCBFAD106AA11" clone="SCBFAD106AA11" clone="SCBFAD106AA11" clone=lib="AD1" clone="SCBFAD106AA11" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="AD1" clone=lib="Clone=lib="AD1" clone=lib="AD1" clone	Query Match 65.0%; Score 503; DB 6; Length 647; Best Local Similarity 86.8%; Pred. No. 2.6e-92; Antiches 567; Conservative 0; Mismatches 80; Indels 6; Gaps 1; Qy 104 GCCGTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 164 CGAACGTGGCTAATGTGGTCACCGACGCTTCTTCAACGGCATCAAGAACCAGGCCGGGA 223 Db 61 GGAACGTGGCTTGTCACCGACGCATTCTTCAACGGCATCAAGAACCAGGCCGGGA 120 Qy 224 GCGGGTGCGAGGCGCAACACTCTACACCCGGGGGTTCCTCGAGGCCATCGCGGGT 283 Db 121 ACGGTGCGAGGGCGAACACTTCTACACCCGGAGGGCGTTCCTCGAGGCCATCGCGGCGT 180	284 181 344 235	404 ACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGGCGCGGGGCAGAAGTACTACG	0y 524 GCTTCCACGGGACCCCGGCAGGGGGGGGGGGGGGGGGGG	OY 704 CGCGCTCGGCTACACAGCAGTACTCCCGCCAGCTCGGCGTCGACCCGGGC 756
186 CGACGCGTTCTTCAACGCATCAAGAACCAGGCCGGAAGCGGGTGCGAGGGCAAGAACTT 245 283 CGACGCATTCTTCAACAGCATCAAGAACCAGGCCGGGAACGGGTGCGAGGGCAAGAACTT 342 246 CTACACCCGGAGCGCTTCCTCGAGGCCATCCCCGGCTACCCGGCTTCGCGCAAGACTT 342 343 CTACACCCGGAGCGCTTCCTCGAGGCCATCCCCGGCTTCGCGCATCGCGCATGGCGG 305 344 CTACACCCGAAGCGCAACTCCTCAGCGCCACCCGACGCGTTCGGTGG 396 306 CTCCGAGGTCGAGCGCAAGATGCCGCCCTTCTTCGCGCACGCCACGCACG	ATCTC GACCC HILL AACCC ATGAA	637 GGACAGGGGGCAAGACGCCGTGGTCGCGTTCAAGACGGCGCTCTGGTTCTGGACCAA 696 606 CAACGTGCACCGTGTGATGCCGCAGGGCTTCAGGGCCATCAACGGCC 665 607 CAACGTGCACGGGTGATGCCGCAGGGTTCGGCCCACCATCAAGGCCATCAACGGCGC 756 666 CCTCCAGTGCAACGGGAACAACCCGCCCACCACCACCACCACCACCAC	757 CCTCGAGTGCAACGCAAATACTGCCCAGATGAACGCGGGGGGGG	5 5	itae; Streptophyta; Emt. Liophyta; Liliopaida; Endropogoneae; Saccharu: ra,F.R., Kemper,E.L. ar de SUCEST (1-4), 1-7 (2001) blecular e Engenharia G clec Campinas	Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1137 Eaxis 55 19 3788 1089 Email: parruda@unicamp.br Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 067 row: A column: 11 Seq primer: T7 Promoter Primer. Location/Qualifiers

RESULT 10 CA197556 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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CD995497 820 bp mRNA linear EST 16-JUL-2003
QBB55£07.xg QBB Zea mays CDNA clone QBB25£07, mRNA sequence.
CD995497
                                  647 CGGCAGGGTGGCGCGCGGGCGGTGGTGGTCAAGGCGGCGCTCTGGTTCTGGATGAA 706
                                                                                                                                                                                                                                                                                                               Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 820)
Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infoblogen.fr).
Location/Qualifiers
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Pred. No. 6.7e-92;
0; Mismatches 35; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/tlssue_type="embryo"
/clone_lb="QBB"
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Best Local Similarity 93.7%;
Matches 522; Conservative 0
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                                                             SM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 710)

S Lai, J. Dev, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,

Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its

comparison to the rice genome

L Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinsheng

Dr. Joachim Messing's lab

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/culfitvar="W23"
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/clone_lib="Taxon:pt 8K-; Site_1: BcoRI; Site_2:
//note="Vector: pBluesGript 8K-;
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.larity 91.2%; Pred. No. 4.2e-92;
Conservative 0; Mismatches 35,
                                                                                                                                                                                                                                                                                                                                                Email: jlai@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
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Location/Qualifiers
                    GI:31359135
CD443492
CD443492.1
BST.
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Matches 551; Conserv
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QBB18407.xg QBB Zea mays cDNA clone QBB18407, mRNA sequence.
61 TACCCAGGCTTCGCCCACGGGGGGCGAGGTGCAGGGCAGGCGAGGCAGAGCGCGGAATCGCCGCCTTC 120
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1 (Sases I to 741)
Genoplante.
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93, rue Henri Rochefort 91025 EVRY CEDEX France
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/tissue_type="embryo"
/clone_lib="QBB"
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                                     405 GTTCAAGGCGGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGGTGGTGCCGCAGGGGTC 464
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Location/Qualifiers

1. .578

Corganiam="Zea mays"

And type="man"

(cultivar="RaNA"

(cultivar="Raxon:457"

/db xref="taxon:457"

/clone="QBB15f08"

/tissue type="embryo"
/clone_lib="QBB15f08"
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Contact: Genoplante
Genoplante
          GTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCCGCAGGGCTT
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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TTCGCGCACGCCACGCACGAGCCGGCCATTTCTGCTACATCAGCGAGATCAACAAGAGC 180
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
Genoplante
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| organism="Zea mays" |
| organism="Zea mays" |
| mol_type="mRNA" |
| cultivax="P2" |
| db_xref="taxon:4577" |
| clone="QBB18e05" |
| clone="Ib="QBB" |
| clone="Ib="QBB" |
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nucleic search, using sw model OM nucleic

Run on:

May 23, 2005, 14:20:22 ; Search time 397.391 Seconds (without alignments) 11943.947 Million cell updates/sec

US-10-692-367-11 774 Perfect score:

1 tegatgeagaactgeggetg......geaacaaceteacetgetga 774 Sequence:

Scoring table:

5695437 seqs, 3066160638 residues Searched:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

11390874

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*

/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* ptodata/2/pubpna/US10_NEW_PUB.seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

!	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
	11,	11,	29,	33,	29,	33,	71,	45,	45,	23,	29,
Description	Sequence 1	Sequence 1	Seguence	Sequence			-			Sequence	Sequence
ΩΙ	US-10-692-367-11	US-10-389-432B-11	US-10-692-367-29	US-10-692-367-33	US-10-389-432B-29	US-10-389-432B-33	US-10-692-367-71	US-10-692-367-45	US-10-389-432B-45	US-10-692-367-23	US-10-692-367-59
80	19	18	19	19	18	18	19	19	18	19	19
& Query Match Length DB	774	771	774	774	771	771	774	774	771	774	771
Query Match	100.0	9.66	98.3	98.1	98.0	97.8	94.0	92.4	92.0	91.9	91.7
Score	774	771	761.2	759.6	758.2	756.6	727.6	714.8	711.8	711.6	710
Result No.	-	7	m	4	'n	9	7	α,	σ	10	11

Sequence 37, Appl Sequence 23, Appl Sequence 59, Appl Sequence 37, Appl Sequence 61, Appl Sequence 65, Appl	Sequence 61, Appl Sequence 65, Appl Sequence 63, Appl Sequence 47, Appl Sequence 63, Appl Sequence 64, Appl	Sequence 73, Appl Sequence 30480, A Sequence 135817, Sequence 67, Appl Sequence 67, Appl Sequence 83, Appl		410041661
10-692-367- 10-389-432B 10-389-432B 10-389-432B 10-692-367- 10-692-367-	US-10-389-432B-61 US-10-389-422B-65 US-10-692-367-63 US-10-692-367-47 US-10-389-432B-63 US-10-389-432B-47	10 - 692 10 - 425 10 - 692 10 - 692	10-69 10-38 10-69 10-69 10-69	2-367 2-367 2-367 9-432 9-432 9-432 2-367 5-115
118 118 119	18 11 18 18 18	19 17 18 19 19	19 18 19 19	19 118 118 118 118
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708.6 707 707 706.8 706.8	703.8 703.8 703.6 702 700.6 699	691.8 691.8 691.8 690.8 686.8	682.8 680.4 679.8 677.4 677.2	674.8 674.6 674.2 673.4 671.8 669.4 668.4
113 114 116	18 20 22 23 23	25 25 26 27 29	0 H W W W W W W W W W W W W W W W W W W	W W W A A A A A A A A A A A A A A A A A

ALIGNMENTS

Sequence 11, Application US/10692367
Publication No. US2005005055A1
GENERAL INFORMATION:
APPLICANT: Multer, Mathias L.
APPLICANT: Simmons, Carl R.
FILE OF INVENTION: MCWEER: US/10/692,367
CURRENT APPLICATION NUMBER: 10/389,432
FRIOR PELING DATE: 2003-10-24
FRIOR PELING DATE: 2003-11-06
FRIOR PELING DATE: 2002-11-06
FRIOR PELING DATE: 2002-11-06
FRIOR PELING DATE: 2002-11-07
FRIOR FILING DATE: 2002-11-07
FRIOR FRIOR PRIOR FRIOR F

TYPE: DNA ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Variant sequence produced by shuffling techniques

, NAME/KEY: CDS , LOCATION: (1)...(774) US-10-692-367-11

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; Sequence 29, Application US/10692367; Publication No. US2005050595A1
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               Length 774;
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Publication No. US20040250309A1
GENERAL INFORMATION:
APPLICANT: Muller, Mathias
APPLICANT: True, Thom
APPLICANT: True, Thom
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
FILE REPERENCE: 488492000300
CURRENT PILIGED DATE: 2003-03-14
CURRENT PILIGED DATE: 2003-03-14
FRIOR APPLICATION NUMBER: 60/337,029
               100.0%; Score 774; DB 19;
100.0%; Pred. No. 1.1e-184;
iive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
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                                                               TYPE: DNA

CRCANISM: Unknown

FEATURE:

7 OTHER INFORMATION: Variant sequence produced by shuffling techniques

CONTENT OFHER INFORMATION: x2C2 nucleic acid

US-10-389-432B-11
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                                                                                                                                                                            Length 771;
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                                                                                                                                                                            Query Match
99.6%; Score 771; DB 18; L
Best Local Similarity 100.0%; Pred. No. 6.2e-184;
Matches 771; Conservative 0; Mismatches 0;
                                                                                                                                                                                                         ;
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 771
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541 GACCCCGGCAGGGTGGCGCGGGACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGG 600
                                                                                         61 ACGACCGACGACGACGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AACTICTACACCCGGAGCGCGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AACTICTACACCCGGAGCGCGTICCTCGAGGCCAICGCCGCGTACCGGGCTICGCGCAI 300
                                                                                                                                                                        ACAACCGACGAGTACTGCGGCGACGAGTGCCAGTCGGGCCCGTGCCGTCGGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GECACCGACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGCGGCGGCGGCGGCGGCGGCGCGCGCAGGCAGCCGCGCGGTGCGAACGTGGCTAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCGATGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                             721 AGGCAGTACTGCCGCCAGCTCGGCGTCGACCGGGCAACAACCTCACCTGCTGA 774
                                                                                                                                                                                                                                                                                                                                     721 AAGCAGTACTGCCGCCCAGCTCGGCGTCGACCCCAGGCCCCAACCTCACTTGCTGA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Variant sequence produced by shuffling techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MILIER, Mathias L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: World Compositions with chitinase
TITLE OF INVENTION: activity
FILE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: 10/389,432
PRIOR FILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 90/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 100/337,029
PRIOR PILING DATE: 2002-10-22
INUMBER OF SEQ ID NOS: 84

LENGTHAR: PastSEQ for Windows Version 4.0
SEQ ID NO 33
PRIOR PILING DATE: 2002-10-22
IENGTHAR: PastSEQ for Windows Version 4.0
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Pred. No. 4.5e-181;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/10692367; Publication No. US20050050595A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.1%;
98.8%;
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Best Local Similarity 98.8
Matches 765; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(774)
US-10-692-367-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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                                                          601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AcGACCGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCGCTGCCGCTCGGGCGGCGCGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGCGGCGCCGCCGCGCGCCGCCGCGCGAGCCAGTGGCCGTGCGAACGTGGCTAATGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGCGGCGGCGGCGGCGGCGGCGGCGGAGCCAGTGGCGGTGCGAACGTGGCTAATGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCACCGACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGCCAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTICIACACCCGGAGGGGGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AACTICTACACCCGGAGCGCGTICCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCCGCCTTCTTCGCGCACGCCACGCAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCCGCCTTCTTCGCGCACGCCACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCCTACTGCGACCCG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAAGAGGCAGTGGCCCGCGCGGGGCAGAAGTACTACGGGCGCGGCCCGCTGCAG 480
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OTHER INFORMATION: Variant sequence produced by shuffling techniques
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                                    APPLICANT: FILTE, FRACTION APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
ITILE OF INVENTION: Novel compositions with chitinase
ITILE OF INVENTION: Activity
ITILE OF ILING DATE: 2003-11-06
INTOR FILING DATE: 2001-11-07
INTORE FILING DATE: 2001-11-07
INTOREMENT OF SEQ ID NOS: 84
SOOTWARE: FARENCE OF SEQ ID NOS: 84
INTOR FILING DATE: AND ACTIVITY
INTOREMENT OF SEQ ID NOS: 84
SEQ ID NO 29
INTOR INTOREMENT OF SEQ ID NOS: 84
INTOR INTOREMENT OF SEQ ID NOS: 84
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-29
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GOCGCTCCGAGGTCGAGCGCAAACGCGCGATTGCCGCCTTCTTCGCGCACGCCACGCAC
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                                                                                                                                                                                                                                                                                                                                                    541 GACCCCGGCAGGGTGGCGCGGGGACGCCGTGGTGGTGTCAAGGCGGCGCTCTGGTTCTGG
                                                                                                                            241 AACTICTACACCCGGAGCGCGTICCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT
                                                                                                                                                                                                                                                            361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCCTACTGCGACCCG
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                                                              GTCACCGACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGCTGCGAGGGGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                               481 ATCTCGTGGAACTACAACTACGGCCCCGCGGGGAGGGCCATCGGCTTCGACGGCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Variant sequence produced by shuffling techniques ; OTHER INFORMATION: rl AG9 nucleic acid US-10-389-432B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18; Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/10389432B

Publication No. US20040250309A1

Publication No. US20040250309A1

GENERAL INFORMATION

APPLICANT: Simmons, Carl

APPLICANT: True, Thom

APPLICANT: True, Thom

APPLICANT: Standani, Nasser

TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE

TITLE OF INVENTION: ACTIVITY

FILE REFERENCE: 48942200300

CURRENT APPLICATION NUMBER: US/10/389,432B

CURRENT APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 771
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ORGANISM: Unknown
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US-10-389-432B-33
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                                     GGCGGCTCCGAGGTCGAGCGCAAGCGCGAATTGCCGCCTTCTTCGCGCACGCCACGCAC
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US-10-389-4328-29
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98.0%; Score 758.2; DB 18; Length
Best Local Similarity 99.0%; Pred. No. 1e-180;
Matches 763; Conservative 0; Mismatches 8; Indels
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US-10-389-432B-29
Sequence 29, Application US/10389432B
Sequence 29, Application US/10389432B
Publication No. US20040250309Al
Sequence 29, Application US/10389432B
SENERAL INFORMATION:
APPLICANT: Muller, Mathias
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 489492000300
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT FILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 771
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ORGANISM: Unknown
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Pred. No. 4.8e-173;
0; Mismatches 29;
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 774
                                                                                                                                                                                                                             94.0%;
                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 96.3<sup>3</sup>
Matches 745; Conservative
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; LOCATION: (1)...(774)
US-10-692-367-71
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                                                      1 TCGATGCAGAACTGCGGCTGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGGC
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Publication No. US2005005055A1

GENERAL INFORMATION

APPLICANT: Miller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: activity

FILE REFERENCE: 54916200320

CURRENT FILING DATE: 2003-10-22

FRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/390,086
98.8%; Pred. No. 2.6e-180;
ive 0; Mismatches 9;
             762; Conservative
Best Local Similarity
Matches 762; Conserv
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US-10-692-367-71
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                                                                           APPLICANT: Mathias L.
APPLICANT: Mathias L.
APPLICANT: ATTLE, Mathias L.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Stalpani, Nosel compositions with chitinase TITLE OF INVENTION: Novel compositions with chitinase TITLE OF INVENTION: Activity FILE REPERSES: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT PELING DATE: 2003-10-2
PRIOR FILING DATE: 2003-10-4
PRIOR FILING DATE: 2002-11-06
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PELING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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92.4%; Score 714.8; DB 19
Best Local Similarity 95.2%; Pred. No. 7.9e-170;
Matches 737; Conservative 0; Mismatches 37;
                                     Sequence 45, Application US/10692367
Publication No. US20050050595A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ... (774)
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; NAME/KEY: CDS
; LOCATION: (1).
US-10-692-367-45
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                                 481 ATCTCGTGGAACTACAACTACGGGCCGCGGGGAGGGCCATCGGCTTTGACGGCTCGGG
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                                                                                          GACCCCGGCAGGGTGGCGCGGGGACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGG
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CTHER INFORMATION: Variant sequence produced by shuffling techniques
CTHER INFORMATION: 4N1/80_F8 nucleic acid
US-10-389-432B-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/10389432B
Publication No. US20040250309A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Miller, Mathias
APPLICANT: Miller, Mathias
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: ABJEAN: NOVEL COMPOSITIONS WITH CHITINASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 48949200300
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
SPRIOR PRING DATE: 2001-11.07
SOFTWARE: PRESECT FOR WINDOWS VERSION 4.0
SEQ ID NO 45
LENGTH: 771
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Best Local Similarity 95.2
Matches 734; Conservative
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ORGANISM: Unknown
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US-10-389-432B-45
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241 AACTICIACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCAT 300
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   1 TCGATGCAGAACTGCGGCTGCCAAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
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Sequence 59, Application US/10692367

Publication No. US2005005055A1

GENERAL INPORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: True, Thom

APPLICANT: True, Thom

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: NOVEL CONDOCT

CURRENT FILING DATE: 2003-10-22

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/290,086

PRIOR PILING DATE: 2003-11-06

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2002-11-07
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Pred. No. 5e-169;
0; Mismatches 39; Indels 0;
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Sequence 23, Application US/10692367

Publication No. US2005005055A1

GENERAL INFORMATION:

APPLICANT: Mimmons, Carl R.

APPLICANT: Simmons, Carl R.

FILE OF INVENTION: Novel compositions with chitinase

CURRENT PELING DATE: 2003-10-22

CURRENT PILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 774
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Best Local Similarity 95.0%;
Matches 735; Conservative (
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; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-23
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US-10-692-367-23
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                                                                                        OTHER INFORMATION: Variant sequence produced by shuffling techniques
                                                                                                                                                                                      3;
                                                                                                                                                              Length 771;
                                                                                                                                                              Query Match 91.7%; Score 710; DB 19; Length 7 Best Local Similarity 95.7%; Pred. No. 1.3e-168; Matches 741; Conservative 0; Mismatches 30; Indels
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 771
                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-10-692-367-59
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RESULT 12 US-10-692-367-37 ; Sequence 37, Application US/10692367

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                               GENERAL INFORMATION:
APPLICANT: HIPOGRAFILO.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Activity
FILE REFERENCE: 549162000320,
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2002-10-22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 91.7%; Score 710; DB 19; Local Similarity 94.8%; Pred. No. 1.3e-168; es 734; Conservative 0; Mismatches 40;
Publication No. US20050050595A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-37
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Pred. No. 7.1e-168;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gequence 59, Application US/10389432B

publication No. US20040250309Al

publication No. US20040250309Al

GENERAL INFORMATION:

APPLICANT: Milmen, Carl

APPLICANT: True, Thom

APPLICANT: True, Thom

APPLICANT: Yalpani, Nasser

TITLE OF INVENTION: ACTIVITY

FILE REFERENCE: 48949200030

CURRENT APPLICATION NUMBER: US/10/389,432B

CURRENT APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 2001-11-07

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 59

LENGTH 7.88
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Best Local Similarity 95.7%;
Matches 738; Conservative 0
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ORGANISM: Unknown
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AACTICIACACCCGGAGGGGGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT
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                                                         ATGAACAACGTGCACCGTGTGATGCCGCAGGCTTCGGCGCCCACCATCAGGGCCATCAAC
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94.9%; Pred. No. 2.8e-168;
iive 0; Mismatches 39; Indels
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US-10-389-432B-23

Sequence 23, Application US/10389432B

Publication No. US20040250309A1

GENERAL INFORMATION:
APPLICANT: Malhas
APPLICANT: Simmons, Carl
APPLICANT: True, Thom
TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
FILE REPERENCE: 489492000300
CURRENT FILING DATE: 2003-03-14
PRIOR PILING DATE: 2001-11-07
NUMBER OF SEQ. ID NOS: 66
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 771
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Best Local Similarity 94.9
Matches 732; Conservative
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ORGANISM: Unknown
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Best Local Similarity
Matches 731; Conserv
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ORGANISM: Unknown
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US-10-389-432B-37
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Sequence 5 Sequence 9 Sequence 9 Sequence 9 Sequence 1 Sequence 2

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Sequence 3

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CGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGCGGTGGCGG
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APPLICANT: Simmons, Carl R.

APPLICANT: Salmons, Carl R.

TITLE OF INVENTION: Maize Chitinases and Their Use in

TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

FILE REPERENCE: 1100

CURRENT APPLICATION NUMBER: 05/09/522,714

CURRENT FILING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/125,915

EARLIER PILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%; Score 647.8; DB 4;
91.8%; Pred. No. 3.1e-112;
ive 0; Mismatches 42;
US-09-534-229C-8
US-09-522-714-23
US-09-522-714-5
US-08-812-025-9
US-08-812-025-9
US-09-138-873-9
US-09-522-714-17
US-09-522-714-17
US-09-522-714-13
US-09-522-714-13
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US-09-523-714-13
US-08-449-315-38
US-08-449-315-38
US-08-449-315-38
US-08-449-03-38
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; Sequence 1, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
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Matches 704; Conservative
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US-09-522-714-1
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ORGANISM: Zea mays
         110.77
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APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/125,915
BARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (42)...(854)
US-09-522-714-21
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US-09-522-714-29
i Sequence 29. Application US/09522714
j Betent No. 6563020
j GENERAL INFORMATION:
j APPLICANT: Simmons, Carl R.
j APPLICANT: Valpani, Nasser
j TILE OF INVENTION: Balancing Disease Resistance in Crop Plants
j TILE OF INVENTION: Enhancing Disease Resistance in Crop Plants
j CURRENT APPLICATION NUMBER: US/09/522,714
j CURRENT FILING DATE: 2000-03-10
j EARLIER PILING DATE: 1999-03-24
j NUMBER OF SEQ ID NOS: 32
software: PastSEQ for Windows Version 3.0
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Best Local Similarity 80.71
Matches 453; Conservative
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) LOCATION: (3)...(551)
US-09-522-714-29
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                                CGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGCGGCGGCGGTGCCGG 125
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                                                    Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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GENERAL INFORMATION:
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                CTACACCGGGGGGGGGGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCATGGCGG
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APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Males Chitinaees and Their Use in
TITLE OF INVENTION: Males Chitinaees Resistance in Crop Plants
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT FILING DATE: 2000-03-10
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 31
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38.3%; Score 296.8; DB 4; Length 1116;
Best Local Similarity 65.7%; Pred. No. 8.6e-47;
Matches 556; Conservative 0; Mismatches 177; Indels 113;
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Patent No. 6563020
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NAME/KEY: CDS
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ORGANISM: Zea mays
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NAME/KEY: intron
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APPLICANT: Spaine, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRILING DATE:

PRILING DATE:

16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

10 07/937,197

FILING DATE:

APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NU
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FILING DATE: 20-0CT 1989
FRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
FRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/768,122
FILING DATE: 7-SEP-1991
FRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
FRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
FRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580, 431
FILING DATE: 20-UIN-1989
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION
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ATTORNEY/ABOTT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                            Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hawthorne CTIY: New Tree CTIY: CITY: Hawthorne
Moyer, Mary B.
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
: USA
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                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTA 527
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                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                          Length 1079;
                                                                                                                                                                                                                                        Score 174.6; DB 1; Length : Pred. No. 5.2e-24; 0; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           153 GATGCATACTGCGCTGTTGGATGCCGATCAGGTCCTTGTA----
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; Sequence 37, Application US/08449315
; Patent No. 5650505
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                            Query Match 22.6%;
Best Local Similarity 56.5%;
Matches 436; Conservative
                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-449-315-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                            APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
DELON NUMBER: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-304-94
APPLICATION NUMBER: 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/0/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
FILOR APPLICATION DATA: 1988
FILING DATE: 6-MPR-1993
FILING DATE: 6-APR-1993
FILING DATE: 6-APR-1993
FILING DATE: 21-DEC-1990
FILING DATE: 21-DEC-1990
FILING DATE: 20-CCT 1989
FILING DATE: 20-CCT 1989
FILING DATE: 6-MAR-1992
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
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27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CIBA-GEIGY Corporation
                                                           Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Melns, Jr., Frederick
Montoya, Alice
                                                                                                                                               Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
               Alexander, Danny C
                                 Beck, James J.
Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
John A
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PRIOR APPLICATION
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                             APPLICANT:
APPLICANT:
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APPLICANT:
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247 TACACCCGGAGCGCTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGGCATGGCGGC 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGTGGCGGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGGCAGGGGGCGCGGGACGCCGTGGCGTTCAAGGCGGCCCTCTGGTTCTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

22.6%; Score 174.6; DB 1; Length 1079;
Best Local Similarity 56.5%; Pred. No. 5.2e-24;
Matches 436; Conservative 0; Mismatches 284; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTA-----
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-193
ATTORNEY/AGRIT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE DOCKET NUMBER: 36,129
TELECOMUMICATION INFORMATION:
TELECOMUMICATION INFORMATION:
TELECOMUMICATION INFORMATION:
TELECOMUMICATION INFORMATION:
TELECOMUMICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 10/19 base pairs
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93 caaaacrigceerreceaaaccrererrecaercaerrecerraerrecerraereceae 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGTGGCGGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 GACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGCGGGGGGCAAGAACTTC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 racaccegreacrerricerracececeraaracririceceaacrireceaarrecear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 TCGTGGAACTACAACTACGGGCCCCGCGGGAGGCCCATCGGCTTCGACGGCCTCGGGGAC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 caagerincirraacaararrarcaaccaaccreeraareerrececeeesaaaaarre 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 GGACATTTCTGCTACATAGAAGATTAACGGAGCAACACGTAACTACTGCCAGAGCAGC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.6%; Score 174.6; DB 1; Length 1079; Best Local Similarity 56.5%; Pred. No. 5.2e-24; Matches 436; Conservative 0; Mismatches 284; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 GATGCATACTGCGTGTTGGATGCCGATCAGGTCCTTGTA----
                PRICATION NUMBER: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1990
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
REGISTRATION NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
METERSPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-444-803-37
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724 CAGTACTGCCGCCAGCTCGGCGTCGACCCGGGCAACAACCTCACCTGCTGA 774
                                                                                                                                                      765 gacrarricregacagerregrerececeregrecraacerragriecraa 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER KEALALE FORM:
COMPUTER: TEMPER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 1-JAN-94
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-D-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
FILING DATE: 1-APR-199
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08444803
Patent No. 5654414
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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67 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGGCGGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 -------Galgeracrecaacceacceacedacercecrecacecrecaracearrere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 CAAGGTITCTITAACAATATTATCAACCAAGCTGGTAATGGTIGCGCGGGAAAAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 GACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGGTGCGAGGCAAGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.6%; Score 174.6; DB 1; 56.5%; Pred. No. 5.2e-24; iive 0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-19825/P1/CGC 1727
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
PILING DATE: 8-MAR-1989
PRIOR APPLICATION NUMBER: US 07/165,667
PILING DATE: 8-MAR-1989
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 6-APR-1933
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/68,506
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/68,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIMER: Jamee SCOCT
REGISTRATION NUMBER: S-19825/P1/
TELERORMUNICATION NUMBER: S-19825/P1/
US 07/305,566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1079 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.5
Matches 436; Conservative
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Si
TOPOLOGY: linear
MOLECULE TYPE: DNA
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APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Sperison, Christoph
APPLICANT: Sperison, Offirey R.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Walliams, Scott J.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REQULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DAM SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             765 gácriárricregaciagérricgregacecregerecriadecria 815
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRICK APPLICATION NUMBER: 08/181,271
FILING DATE: 16-UL-1993
FILING DATE: 16-UL-1993
PRICK APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UL-1993
PRICK APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UL-1993
FILING DATE: 16-UN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/08449043
Patent No. 5689044
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
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Length 1079; Indels

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; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-456-265A-37
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588 ccccaactrorccaacccaacroraccrircaccroccccarrorccirricacarc
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GENRRAL INFORMATION:
APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: Grinson, Jeffrey R.
APPLICANT: Grinson, Jeffrey R.
APPLICANT: TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTATTGTGGACAGCTTGGTGGACCCTGGTCCTAACCTTAGTTGCTAA
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION:
435
PRIOR APPLICATION:
APPLICATION NUMBER:
US 08/181,271
PILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
THING APPLICATION NUMBER:
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BRIOR APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5767369
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93 CAAAACTGCGGTTGCGCTCCCAAACCTCTGTTGCAGTTCGGTTACTGTGGGTACCGAC 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 ------GAGGTAGTGGAACCCCGACCGGAGGGTCGGTCGGTAGCATTGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GACGCGTTCTTCAACGGCATCAAGAACCAGGCGGGAGCGGGTGCGAGGCAAGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAAGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 gargcaracrecegrerregarecegarcaegrecriera----
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 8-FAR-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 1-DEC-1990
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/569,431
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/569,431
FILING DATE: 27-SEP-1990
PRIOR APPLICATION NUMBER: US 07/569,672
FILING DATE: 27-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 28-US-1990
PRIOR APPLICATION NUMBER: US 07/369,672
FILING DATE: 24-WAR-1889
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%;
56.5%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1079 hard
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Best Local Similarity 56.5
Matches 436; Conservative
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08/181,271
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Best Local Similarity 56.5%;
Matches 436; Conservative
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TELEPAC. (919)541-8689
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (919)541-8614
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                     APPLICATION NUMBER: 08/
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US
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STRANDEDNESS: sing
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467
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                                                                                                                                                                                                                                                                                                                                                                                           648 AATAGCGTAAGGCCGGTTCTGAACCAAGGTTTGGAGCCACCATTAGAGCTATTAATGG- 706
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                                                        707 -- AATGGAATGTAACGGTGGTAATTCCCGTGCAGTCAACGCAATGGATAGTACTATAGA 764
                                                                                           408 GGACATTTCTGCTACATAGAAGAGATTAACGGAGCAACACGTAACTACTGCCAGAGCAGC
                                                                                                                                                                                                                                                                               CCCGGCAGGGTGGCGCGGACGCCGTGGTGCGTTCAAGGCGGCGCTCTGGTTCTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          724 CAGTACTGCCGCCAGCTCGCCGTCGACCGGGCAACAACCTCACCTGCTGA 774
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APPLICANT: Williams, Shericas C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIBA-GRIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander, Danny C.
Beck, James J.
Puesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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Neuhaus, Jean-Marc
Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG'
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US-08-455-416-37
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APPLICANT:
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APPLICANT:
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APPLICANT:
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67 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGTGCCGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 chahacrecedriececrechahecrerieriecherekirekirekiracrereteraecae 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILTURE AND ADDRAY PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/580,431
FILLING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/586,672
FILLING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILLING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILLING DATE: 12-APR-1993
APPLICATION NUMBER: US 08/045,957
FILLING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elner, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.6%; Score 174.6; DB 1; 56.5%; Pred. No. 5.2e-24; tive 0; Mismatches 284;
                     PRILING DATE: 16-UL-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
PILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
PRIOR APPLICATION NUMBER: US 07/165,667
PRIOR APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICATION DATA:

APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRICA APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1999
PRICA APPLICATION NATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-MAR-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRICA APPLICATION NUMBER: US 07/768,122
US 08/093,301
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22.6%; Score 174.6; DB 1; Length 1079;
                                                                                                                                                                                     OPERATING SYSTEM: EV-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIPICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
FILING APPLICATION NUMBER: US 08/093,301
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-MAY-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/68,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/68,566
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1998
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1998
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1998
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 1-APR-1999
PRIOR APPLICATION NUMBER: US 07/68,122
PRIOR APPLICATION NUMBER: US 07/680,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                      ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE:
US-08-455-244-37
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240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAGATTC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 CCCGAACTIGIGGGTACCAACTGTAGCTTTCAGGTCGGGTTTGTGGTTTTGGATG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AACAACGIGCACCGIGIGAIGCCGCAGGGCIICGGCGCCACCAICAGGGCCAICAACGGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 AATAGCGTAAGGCCGGTTCTGAACGATGGTTTGGAGCCACCATTAGAGCTATTAATGG- 706
                                                                                          187 GACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTC 246
                                                                                                                                                                                                          247 TACACCCGGAGCGCGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCATGGCGGC 306
                                                                                                                                                                                                                                                                                                                         408 ggacarricriscriacaragaagarriaacgaaggaagcaacacgraacracrisccagagcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 AAGAGGCAGTGGCCCCCCCCCCGCGGGCAAGTACTACGGGCGCGCCCCCCTGCAGATC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTGGAACTACAACTACGGGCCCGCGGGGGGGGCCATCGGCTTCGACGGGCTCGGGGAC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGGCAGGGTGGCGCGGCACGCCGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 TÁCACCCGTGACTCTTTCGTTAACGCCGGTAATACTTTCCCCAACTTTGCCCAATTCTGTT 359
                                                                                                                                                                                                                                                                                                                                                                                360 AC------CAGACGTGAATTGCTACCATGTTTGCTCATTTCACTCACGAGACC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                         707 --aarggaargraacggragraarrccggrgcagrcaacgcaaggarrggaracraraga 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                765 GACTATTICTGCACACCTTGCACCCTGCTCCTAACCTTAGTTGCTAA 815
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander, Danny C. Beck, James J. Duesing, John H. Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice Moyer, Mary B. Neuhaus, Jean-Marc Payne, George B. Sperison, Christoph Stinson, Jeffrey R. Uknes, Scott J. Mard, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/08455244 Patent No. 5789214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals, John A.
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Stinson, Jeffrey R.
APPLICANT: Wines, Scott J.
APPLICANT: Wines, Scott J.
APPLICANT: Wines, Scott J.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: 7 Skyline Drive
CITY: Hawthorne
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 16-701-1993
FILING DATE: 16-701-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-701-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
FILING DATE: 1-APR-1991
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PRIOR PAPLICATION NUMBER: US 07/165,667
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
PRIOR APPLICATION NUMBER: US 07/632,441
PRIOR APPLICATION NUMBER: US 07/632,441
PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/848,506
BTING DATE: 6-MAD-1007
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/300 ""FILING DATE.
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FILING DATE: 27-SEF-122-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 8-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 6-MAR-1992 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy
                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                             240 CAAGGITTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAAGATTC 299
                                                                                                                                                                             GACGAGTACTIGCGGCGACGGGTGCCAGTCGGCCCCCGTGCCGCTCGGCGGCGGTGGCGGC 126
                                                                                                                                                                                                                          127 GGCGGCGGCGCGCGGCGCGCGGCGCGGTGGCGGTGCGAACGTGGCTAATGTGTCACC 186
                                                                                                                                                                                                                                                                                                                             193 -------GAGGTAGTGGAACCCCGACCGGAGGGTCGGTCGGTAGCATTGTGACA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 TCATGGAACTACAACTACGGAGCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
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                                                                             7 CAGAACTGCGGCTGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC 66
                               Gaps
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                             51;
Best Local Similarity 56.5%; Pred. No. 5.2e-24;
Matches 436; Conservative 0; Mismatches 284; Indels
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harne Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
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Patent No. 5804633
GENERAL INFORMATION:
APPLICANT: RYAIS, John A.
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US-08-454-876-37
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Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTR:

ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING PATE: 31-MAY-1995
FILING PATE: 31-MAY-1995
FILING PATE: 31-MAY-1995
FILING PATE: 31-MAY-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
PILING DATE: 6-NOV-1992
PRIOR APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/678,378
PRIOR APPLICATION NUMBER: US 07/678,378
PRIOR APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/305,566
PILING DATE: 6-FEB-1989
PRIOR APPLICATION NUMBER: US 07/305,566
PRILING DATE: 6-FEB-1989
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PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
RROR APPLICATION DATE:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSS:
ADDRESSEB: CIBA-GBIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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APPLICATION DATA: APPLICATION DATA: US 07/632,441
FILING DATE: 21-DEC-1990
PATOR APPLICATION DATA: US 07/425,504
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20-OCT 1989
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Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Bric R.
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APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,3
Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                        Length 1079;
                                                                                                                                                                                                                                                                                      Score 174.6; DB 1; Length 1
Pred. No. 5.2e-24;
0; Mismatches 284; Indels
                             TELEFAX: (919)541-8689;
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
ILMGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-454-876-37
                                                                                                                                                                                                                                                                                        22.6%;
56.5%;
             (919)541-8614
                                                                                                                                                                                                                                                                                                                                        Matches 436; Conservative
                                                                                                                                                                                                                                                                                                                Similarity
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FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672

US-08-457-364-37; Sequence 37, Application US/08457364; Sequence 17, Application US/08457364; Patent No. 5847258; GENERAL INFORMATION:

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707 --AATGGAATGTAACGGTGGTAATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGA 764
                                                                      724 CAGTACTGCCGCCAGCTCGGCGTCGACCCGGGCAACAACTCCTCACCTGCTGA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,666
FILING DATE: 8-MAR-1989
FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
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7 Skyline Drive
                                                                                                                                                                                                                                                                                                                          Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice
                                                                                                                                                                                       ; Sequence 37, Application US/08456262 ; Patent No. 5851766
                                                                                                                                                                                                                                                                                                                                                                                                                                       Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Whee, Scott J.
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, 8 TITLE OF INVENTION: CITILE OF INVENTION: DINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GGCGGCGGCGGCGGCGGCGGCGGCGCGCGGCGGCGAACGTGGCTAATGTGGTCACC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAAGATTC 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 174.6; DB 2; Length 1
56.5%; Pred. No. 5.2e-24;
ive 0; Mismatches 284; Indels
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR.1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INPORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: 3-19825/P1/CGC 1727
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                              TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.6
Best Local Similarity 56.5
Matches 436; Conservative
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                                                                                                                                                                                                                                                 TELEPHONE:
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528 TCATGGAACTACAACTACGGAGCGTGTGGCCAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
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                                      CCCGGCAGGCTGGCGCGGGACGCCGTGGTGGTTCAAGGCGGCGCCTCTGGTTCTGGATG
                                                                                                                      604 AACAACGIGCACCGIGIGAIGCCGCAGGGCIICGGCGCCACCAICAGGGCCAICAACGGC
                                                                                                                                                                                                          588 ccccaactrigiegeraccaacccaactriracactricacercecerrierecair
                                                                                                                                                    774
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                        724 CAGTACTGCCGCCAGCTCGGCGTCGACCCGGGCAACCTCACCTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
DB1OD NONTARED: B00
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/10E ECC
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Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08456240 Patent No. 5856154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
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Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alexander, Danny C.
Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moyer, Mary B.
Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIBA-GEIGY
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ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGTGGCGGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GGCGGCGGCGGCGGCGCGCGCGCGCAGTGGCGGTGCGAACGTGGCTAATGTGTCGTCACC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 ------GAGGTAGTGGAACCCCGACCGGAGGGTCGGTCGGTAGCATTGTGACA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 174.6; DB 2; Length 1
Pred. No. 5.2e-24;
0; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-19825/P1/CGC 1727
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-5EP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%;
56.5%;
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Best Local Similarity 56.5
Matches 436; Conservative
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FILING DATE: 6-FEB-1989
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 20-DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
NAME: BLEET. James SCOCTT
REGISTRATION NUMBER: S-19825/PI/TELECOMMUNICATION NUMBER: S-19824-19825/PI/TELECOMMUNICATION NUMBER: S-19824-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1079 base pairs
TYPE: nucleic acid
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Best Local Similarity 56.5
Matches 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGTGGAACTACAACTACGGGCCCGCGGGGGGCCATCGGCTTCGACGGGCTCGGGGAC
GGACATTTCTGCTACATAGAAGAGATTAACGAGCACAACACGTAACTACTGCCAGAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 AAGAGGCAGTGGCCGTGCGCCGCGGGGCAGAAGTACTACGGGCGCGGCCCGCTGCAGATC
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Search completed: May 23, 2005, 15:37:14 Job time : 125.13 secs

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US-10-692-367-11 Perfect score: Title:

1 tcgatgcagaactgcggctg......gcaacaacctcacctgctga 774 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	Ads92627 Chitinase	Ads92645 Chitinase	Ads92649 Chitinase	Ads92687 Chitinase	_	Ads92639 Chitinase	_	Ads92653 Chitinase	_	_	Ads92679 Chitinase	_	Ads92689 Chitinase	Adj12126 Maize cDN	_	Ads92699 Chitinase	Ads92623 Chitinase	Ads92659 Chitinase	Ads92691 Chitinase	Ads92641 Chitinase
SOMMAKIES		A	ADS92627	ADS92645	ADS92649	ADS92687	ADS92661	ADS92639	ADS92675	ADS92653	ADS92677	ADS92681	ADS92679	ADS92663	ADS92689	ADJ12126	ADS92683	ADS92699	ADS92623	ADS92659	ADS92691	ADS92641
		BB :	13	13	13	13	13	13	13	13	13	13	13	13	13	11	13	13	13	13	13	13
		Length DB	774	774	774	774	774	774	771	774	771	774	774	771	771	840	765	771	774	753	780	765
,	Query	Match	100.0	98.3	98.1	94.0	92.4	91.9	91.7	91.7	91.3	91.3	6.06	90.7	89.5	89.3	88.7	88.6	88.2	87.9	87.6	87.5
		Score	774	761.2	759.6	727.6	714.8	711.6	710	710	706.8	706.8	703.6	702	692.4	690.8	686.8	989	682.8	680.4	678	677.2
	Result	No.	п	7	m	4	S	9	7	60	6	10	11	12	13	. 14	15	16	17	18	19	20

Ads92655 Chitinase	~	н	Ads92619 Chitinase	^	^		Ads92685 Chitinase		Aaa96222 cDNA enco	Ads92647 Chitinase	Ads92693 Chitinase	Ads92695 Chitinase	Ads92673 Chitinase	Ads92637 Chitinase	Ads92665 Chitinase	Ads92669 Chitinase	Ads92643 Chitinase	Ads92621 Chitinase	Ads92629 Chitinase	Ads92625 Chitinase	Ada49298 Maize gen	Adj44871 Plant cDN	Ada70140 Rice gene	Adj11575 Rice DNA
ADS92655	ADS92657	ADS92631	ADS92619	ADS92697	ADS92667	ADS92651	ADS92685	ADS92671	AAA96222	ADS92647	ADS92693	ADS92695	ADS92673	ADS92637	ADS92665	ADS92669	ADS92643	ADS92621	ADS92629	ADS92625	ADA49298	ADJ44871	ADA70140	ADJ11575
13	13	13	13	13	13	13	13	13	m	13	13	13	13	13	13	13	13	13	13	13	σ	12	8	11
780	771	777	777	753	753	753	753	753	1094	753	753	750	753	753	753	753	753	756	756	756	636	636	843	843
87.4	87.2	87.2	86.5	85.6	85.2	85.0	84.4	83.8	83.7	83.6	83.6	83.4	83.4	82.5	82.3	82.1	81.5	77.5	77.3	77.1	64.0	64.0	60.1	60.1
676.4	674.8	674.6	669.4	662.8	9.629	658	653.2	648.4	647.8	646.8	646.8	645.6	645.2	638.8	637.2	635.6	630.8	600.2	598.6	597	495.6	495.6	465	465
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium; Heterodera. Yalpani N; Chitinase variant polynucleotide #5. Muller ML, True T, Simmons CR, (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC. BP 22-OCT-2002; 2002US-0420666P. 06-NOV-2002; 2002US-00290086. 14-MAR-2003; 2003US-00389432. 22-OCT-2003; 2003WO-US033588 ADS92627 standard; DNA; 774 (first entry) WO2004037194-A2. 02-DEC-2004 06-MAY-2004. Synthetic. ADS92627; RESULT 1 ADS92627

WPI; 2004-365417/34. P-PSDB; ADS92628.

New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

Disclosure; SEQ ID NO 11; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The

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ds;
                                                                                                                                                                          WPI; 2004-365417/34.
P-PSDB; ADS92646.
                                                                                                                                                           Muller ML, True T,
                                                                                                                                   (VERD-) VERDIA INC
        gene;
                                                WO2004037194-A2
                                                                                                  22-OCT-2002;
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       Chitinase;
Heterodera.
                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                 ATCTCGTGGAACTACAACTACGGGCCCCGGGGAGGGCCATCGGCTTCGACGGGCTCCGG
                                                                                                                           Gaps
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fungus is from the genus Fusarium. The nematode is from the genus theterodera. The polymucleotides and polypoptides are useful in enha plant resistance to a fungus or nematode. This sequence represents chitinase variant polymucleotide of the invention.
                                                                          ö
                                                         Length 774;
                                          Sequence 774 BP; 139 A; 251 C; 278 G; 106 T; 0 U; 0 Other;
                                                                           Indels
                                                        Query Match (100.0%; Score 774; DB 13; Best Local Similarity 100.0%; Pred. No. 1.1e-121; Matches 774; Conservative 0; Mismatches 0;
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Chitinase variant polynucleotide #12

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plant resistance; fungus; nematode; Fusarium;
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98.3%; Score 761.2; DB 13;
Best Local Similarity 99.0%; Pred. No. 1.6e-119;
Matches 766; Conservative 0; Mismatches 8;
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                           Length 774;
  Sequence 774 BP; 138 A; 251 C; 278 G; 107 T; 0 U; 0 Other;
               Score 759.6; DB 13; Lengtn
Pred. No. 3e-119;
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98.8%;
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Best Local Similarity 98.8
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               GACCCCGGCAGGGTGGCGCGGGACGCCGTGGTCGTCTCAGGCGGCGCGCTCTGGTTCTGG
                                                                                                                                                                                                                           GACCCCGGCAGGCGCGCGGGCGCCGTGGTGCGTTCAAGGCGGCGCTCTGGTTCTGG
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                                                  ATCTCGTGGAACTACAACTACGGGCCCGCGGGGGGCCATCGGCTTCGACGGGCTCGGG
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                                                                                                                                                                                                                                                                AGGCAGTACTGCCGCCAGCTCGGCGTCGACCCGGGCAACAACCTCACCTGCTGA 774
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Heterodera.
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to chitinase polypeptides and the polynucleotides
                                                                                                                                      GACCCCGGCAGGGTGGCGCGGGACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGG
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                                                                                                                                                                                                                                                            gene; ds; plant resistance; fungus; nematode; Fusarium;
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Pred. No. 1.1e-111;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 45; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitinase variant polynucleotide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                         В.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 95.2
Matches 737; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                 Yalpani
                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 71; 197pp; English.
                                                                                                                                                                                                                                   Simmons CR,
                                                                                                                                                                                    VERDIA INC.
PIONEER HI-BRED INT INC.
                                                                                                                     22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                         22-OCT-2003; 2003WO-US033588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 96.3
Les 745; Conservative
                                                                                                                                                                                                                                   True T,
                                                                                                                                                                                                                                                                  WPI; 2004-365417/34.
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                          WO2004037194-A2
                                                           36-MAY-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 91.9%; Score 711.6; DB 13; Local Similarity 95.0%; Pred. No. 3.7e-111; les 735; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                       Yalpani N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 23; 197pp; English.
                                                                                                                                                                                                                                                                                       Simmons CR,
                                                                                                                                                                                          (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC.
                                                          22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
22-OCT-2003; 2003WO-US033588
                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-365417/34.
P-PSDB; ADS92640.
                                                                                                                                                                                                                                                                                       Muller ML, True T,
                                                       22-OCT-2002;
06-NOV-2002;
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     GACCCGGACAGACTGGCGCAGGACCCCGTGTTGTCGTTCAAGTCGGCGCTCTGGTTCTGG 600
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                              ATGAACAACGTGCACCGTGTGTGATGCCGCAGGGCTTTCGGCGCCCATCAGGGCCCATCAAC
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                                                                                                                             774
                                                                                                                                          Chitinase; gene; ds; plant resistance; fungus; nematode; Pusarium;
Heterodera.
                                                                                                                             AGGCAGTACTGCCGCCAGCTCGGCGTCGACCGGGCCAACAACTCACCTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 710; DB 13; Length 771; 95.7%; Pred. No. 6.9e-111; ive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chitinase variant polynucleotide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 59; 197pp; English
                                                                                                                                                                                                                                                                                        Chitinase variant polynucleotide #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   True T, Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 95.7
Matches 741; Conservative
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                                                                                                                                                                                                                                         ADS92675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GGCGGCGGCGGCGGCGGCGGAGGCGGCGGAGGCAGTGGCGGTGCGAACGTGGCTAATGTG 180
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                                      TCGATGCAGAACTGCGGCTGCCAAGCCTATGCTGCAGCAAGTTTGGCTACTGCGGC
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0; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                              Chitinase variant polynucleotide #28.
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                     True T, Simmons CR,
VERDIA INC.
PIONEER HI-BRED INT INC
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GGCGGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCCGCCTTCTTCGCGCACGCCACGCAC
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                                                                                                                         ATCTCGTGGAACTACAACTACGGGCCCGCGGGGAGGGCCCATCGGCTTCGACGGCTCGGG
                                                                                                                                                                                                      ATGAACAACGTGCACCGTGTGATGCCCGCAGGCTTCGGCCCCACCATCAGGGCCATCAAC
                                                                                                                                                                                                                                 GTCACCGACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGCAAG
                                            AACTICIACACCCGGAGCGCGTICCTCGAGGCCATCGCCGCGTACCCGGGCTICGCGCAI
                                                    GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCCTACTGCGACCCG
                                                                                                                                                                                                                                                          AGGCAGTACTGCCGCCAGCTCGGCGTCGACCGGGCAACAACCTCACCTGCTGA 774
                                                                                                                                                                                                                                                                                                                                                          ds; plant resistance; fungus; nematode; Fusarium;
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                                                                                                                                                                                                                                                                                                                                             Chitinase variant polynucleotide #30
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                                                                                                                                                      standard; DNA; 774
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                                                                                                                                                                                                                                                                                                                                                           gene;
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                          encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                    invention relates to chitinase polypeptides and the polynucleotides
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New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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                                                                                                                                                                                                                                                                                                                                                                                                Length 774;
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.3%; Score 706.8; DB 13; Length
Best Local Similarity 94.6%; Pred. No. 2.4e-110;
Matches 732; Conservative 0; Mismatches 42; Indels
                                                                         Claim 4; SEQ ID NO 65; 197pp; English
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                                                     GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCCTACTGCGACCCG
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     GTCACCGACGCGTTCTTCAACGCCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAG
                                    AACTICIACACCCGGAGGGGGGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCAT
                                                                                                  GCCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCCGCCTTCTTCGCGCACGCCACGCCAC
                                                                                                                                                                                                  361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCCTACTGCGACCCG
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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P-PSDB; ADS92664.
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Heterodera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                  774
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Pred. No. 8.3e-110;
0; Mismatches 44;
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                                                                                                                                                                                                            Chitinase variant polynucleotide #29.
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 94.3%;
Matches 730; Conservative C
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                                                                                                                ADS92679 standard; DNA; 774
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P-PSDB; ADS92680.
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                                                           encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a
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                                                 invention relates to chitinase polypeptides and the polynucleotides
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                                                                                                                                                                                                                             3;
 nematode
                                                                                                                                                                                                    Length 771;
                                                                                                                                                                            Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                           35; Indels
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                                                                                                                                                   chitinase variant polynucleotide of the invention.
                                                                                                                                                                                                 Score 702; DB 13;
Pred. No. 1.5e-109;
0; Mismatches 35;
fundae
 against a
                         Claim 4; SEQ ID NO 47; 197pp; English
  resistance
                                                                                                                                                                                                  Query Match 90.7%;
Best Local Similarity 95.1%;
Matches 736; Conservative C
  enhanced
  with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGT
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                                                                                                                                                                           gene; ds; plant resistance; fungus; nematode; Fusarium;
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89.5%; Score 692.4; DB 13;
Best Local Similarity 94.3%; Pred. No. 6.4e-108;
Matches 730; Conservative 0; Mismatches 41;
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                                                                                                                                     Chitinase variant polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC.
BP.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2003; 2003WO-US033588
  771
                                                                                          (first entry)
  ADS92689 standard; DNA;
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                                                                                          02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muller ML,
                                                                                                                                                                                   Chitinase;
                                                                                                                                                                                                             Heterodera
                                                                                                                                                                                                                                                        Synthetic.
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                                               ADS92689;
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This invention relates to a novel method for identifying isolated polynucleotides that are modulated by post-transcriptional gene silencing polynucleotides that are modulated by post-transcriptional gene sypression in plants via PrGS and the trans-activation of homologues genes due to plants via PrGS and the trans-activation of homologues genes derested to crease. The present invention describes clusters of concreased RNA degradation. The present invention describes clusters of concreased RNA degradation. The present invention describes clusters of concreased RNA degradation. The present invention of gene silencing and the polypeptide sequences derived thereof. Where gene expression is altered in response to PrGS. As such, the elucidation of gene silencing concentrations and targeting the suppression of specific plant genes. This polynucleotide sequence is the suppression of specific plant genes. This polynucleotide sequence is a maize cDNA sequence where expression is modulated by gene silencing, given in an exemplification of the invention. NoTE: This sequence does concreased and the polynucleotide described in the printed specification but has been obtained in
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                                                                                                        cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGTGGCGG
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     ä
                                                                                                     New polynucleotide, useful for modulating gene expression within a by posttranscriptional gene silencing.
     Ricke
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     Provart N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%; Score 690.8; DB 11;
larity 93.9%; Pred. No. 1.2e-107;
Conservative 0; Mismatches 47;
  H
     Moughamer
                                                                                                                                                                               Example 15; SEQ ID NO 762; 79pp; English.
     Kreps J,
Katagiri F,
                                                    WPI; 2003-829655/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
  SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
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                        GGCGGCTCCGAGGTCGAGCGCGAGGTTGCCGCCTTCTTCGCGCACGCCACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maize; 88; post-transcriptional gene silencing; PTGS; plant trans-activation; cereal; plant-viral interaction.
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27-MAR-2002; 2002US-0368327P.
04-APR-2002; 2002US-0370620P.
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COOPER B.
GLAZEBROOK J.
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MOUGHAMER J
PROVART N.
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             734
                                                 The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fuaarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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CAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCGCCCACCATCAGGGCCATCAACGGCGC
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                       ds; plant resistance; fungus; nematode; Fusarium;
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Pred. No. 5.6e-107;
0; Mismatches 37; Indels 9;
                                                                                           GIACTGCCGCCAGCTCGGCGTCGACCCGGGCAACAACCTCACCTGC 771
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                                                                                                                                                                                                                                 Chitinase variant polynucleotide #31.
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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al Similarity 94.1%;
728; Conservative
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                                                                                                                                                              ADS92683 standard; DNA; 765
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                                                                                                                                                                                                                                                       Chitinase; gene;
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                                                                 GGCGGCGGCGGCGGCGGCGGCGGCGGCAGGCAGTGGCGGAACGTGGCTAATGTG
                                                                                                                            232 AACTTCTACACCCGAAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCAT
                                                                                                                                                             GGCGCCTCCGAGGTCGAGCGCAAGCGCGAGATTGCCGCCTTCTTCGCGCACGCCACGCCAC
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Search completed: May 23, 2005, 12:57:05 Job time : 363.896 secs

Perfect score:

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Scoring table:

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Minimum DB Maximum DB

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MZECHITA 843 bp DNA linear PLN 27-APR-1993
Zea mays chitinase A (seed chitinase) gene, complete cds.
M84164
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/evidence=experimental
/product="chitinase A"
/protein_id="AaA33444.1"
/db_xref="GI:L68441"
/translation="MANAPRILALGLIALLCAAAGPAAQNCGCQPNFCCSKFGYCGT
TAXYCGAGGGGGRENGGGGGGGGGGGGGGGANVANVYTDAFFNGIKNQAGSGCG
KNFYTRSAFLSAVNAYPGFAHGGTEVEGKREIAAPFAHTHETGHFCYISEINKSNAY
CDASNRQMPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFNGIAADPNRVAQDAVIAFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases I to 843) Huynh, O.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.
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         AY532777 Zea n
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AY532724 Zea n
AY532716 Zea n
AY53275 Zea n
AY53273 Zea n
AY53272 Zea n
AY53273 Zea n
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Original source text: Zea mays (library: Lamda GT 10 corn
(imbibed)) seed DNA.
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/gene="seed chitinase"
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M84165 Zea mays ch
AY32775 Zea mays
AY32770 Zea mays
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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PLN 27-APR-1993
Maize chitinases and their use in enhancing disease resistance crop plants
Patent: US 6563020-A 1 13-MAY-2003;
Location/Qualifiers
1. 1094
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Pred. No. 1.2e-74;
0; Mismatches 42; Indels 21;
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Matches 704; Conservative
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                                          Score 687; DB 8;
Pred. No. 1.1e-79;
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Sequence 1 from patent US 6563020.
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AR321624.1 GI:33706864
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1 (bases 1 to 1094)
Simmons, C.R. and Yalpani, N.
                                            Query Match 88.8%;
Best Local Similarity 93.5%;
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/traislation="wandaprilalgllallcaaagpaaaonggcoppecskegyggt
TDAYCGDGCOSGPCRSGGGGGGGGGGGGGGGGGGGGANVANVYDAFFNGIKNQAGSGCBG
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ALWFWMNNYHRLMPQGFGATIRAINGALECNGNNPAQMARKGYYKQYCQQLRVDPGP
NLTC"
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Los mays subsp. parviglumis isolate p9 chitinase (chiA) gene, complete cds.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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2 (bases 1 to 1094)

Tiffin,P.

Direct Submission

Submitted (23-JAN-2004) Plant Biology, University of Minnesota,

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

Location/Qualifiers

1. .1094

/organism="Zea mays subsp. parviglumis"
                                                                                                                                                                                                CAGCGTGCACGGGGTGCCGCAGGGTTCGGCGCCACCACCACCAGGCCATGCAACGCGC
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Genetics 167 (3), 1331-1340 (2004)
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Tiffin, P.
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KVGYFGFAHGGSQVQGKREIAAFFAHTHETGHFCYISBINKSNAYOPTKRQMPCA
AGQKYYGKGPLQISWNYNYGPGRAIGEFGEDGLGDPGRVARDAVVAFKAALMFWMNSVHG
VVPQGFGATTRAMQRALECGGNNPAQMNARVGYYRQYCRQLGVDFGPUITC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="PQLVALGLALLCAVAGPAAAQNCGCQPNVCCSKFGYCGTTDEYC
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                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                         1 (bases 1 to 810)

Whyth, Q.K., Hironaka, C.M., Levine, B.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.
Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed J. Biol. Chem. 267 (10), 6635-6640 (1992)
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Pred. No. 2.4e-73;
0; Mismatches 52; Indels 18
                                                                                                                                                                                                                                                                                                     1. .810
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/tissue_type="seed"
/tissue_lib="Lamda GT 10 co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="chitinase B"
/protein_id="AAA33445.1"
/db_xref="GI:168443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 810
/gene="seed chitinase"
/codon_start=1
/evidence=experimental
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Best Local Similarity 90.9%;
Matches 697; Conservative
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Zea mays subsp. parviglumis
Sea mays subsp. parviglumis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                     Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAACTIGCGGCCTAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC
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                                                                 chitinase genes
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                                                                                                                                                               1. .1115
/organism="Zea mays subsp. parviglumis"
/mol type="genomic DNA"
/cultivar="p1184070"
/isolate="p1"
                                                                                                                                                                                                                                                                                                                                                                                                                 72.6%; Score 562; DB 8; L
82.7%; Pred. No. 1.4e-63;
ive 0; Mismatches 50;
                                                               Comparative evolutionary histories of zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
                                                                                                                                                                                                          /sub_species="parviglumis"
/db_xref="taxon:76912"
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/gene="chiA"
join(<24. .456,550. .>953)
/gene="chiA"
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Tiffin, P.
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                                                    CEACGCGTTCTTCAACGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGAGAACTT
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                                       GCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC
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                      Gaps
                      92;
    1094;
   Length
                      Indels
                      52;
    8;
   Score 581.8; DB 8
Pred. No. 3.9e-66;
0; Mismatches 52
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   Query Match
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Matches 715; Conservative
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'gene="chiA"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
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Submitted (23-JAN-2004) Plant Biology, University of
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers

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    .0crganisma"Zea mays subsp. parviglumis"
mol type="genomic DNA"
/cultivar="P1384062"

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/sub_species="parviglumis"
/db_xref="taxon:76912"
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/gene="chiA"
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Zea mays subsp. parviglumis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Tiffin. P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St., Paul, MN 55108-1095, USA
Location/Qualifiers
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                          346 CTACACCCGGAGTGCGTTCCTGAGCGCTCAAGGCGTACCCAGGCTTCGCCCATGGCGG
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FGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGSSSGGGGANVASVVTGSFFNGIKNQA 
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VVAFKAALMFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQYCRQL 
GVDPGPNLTC"
                                                                                                       PLN 29-JUL-2004
complete cds.
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Sea diploperennis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1128)
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                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANCAGAGTACTGCGGCGACGAGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGG
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Pred. No. 1.3e-62;
0; Mismatches 51; Indels 121;
                                                                                                                                                                                                                                                                                       genes in
                                                                                                       linear
(chiB) gene,
                                                                                                                                                                                                                                                                                       chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1128
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                                                                                        AY532740 1128 bp DNA
Zea diploperennis isolate d6 chitinase
AY532740
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Genetics 167 (3), 1331-1340 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Join (14. .470, 592. .995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="chitinase"
                                                                                                                                                 AY532740.1 GI:48093261
              932 AGGCCCAACCTCACTTGCT
GGGCAACAACCTCACCTGCT
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80.6%;
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1094 bp DNA linear PLN 29-JUL-2004 subsp. parviglumis isolate pl3b chitinase (chiA) gene,
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Zea mays subsp. parviglumis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
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2 (bases 1 to 1094)

Tiffin,P.

Direct Submission

Submitted (23-JAN-2004) Plant Biology, University of Minnesota,

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

Location/Qualifiers
812 GGCTTCGGCGCCACCATCAGGCCATCAACGGCGCCCTCGAGTGCAACGGGAACAACCCC
                                                                                                                                                                                  GCCCAGATGAACGCGCGCGTCGGCTACTACAGGCAGTACTGCCGCCCAGCTCGGCGCTCGAC
                                                                                                                                                                                                                          872 GCCCAGATGAACGCGCGCGCGTCGGCTACTACAGCAGTACTGCCAGCAGCAGCTCCGCGTCGAC
                                                                                GGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAACGGGAACAACCCC
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71.4%; Score 552.4; DB 8; Length 1094;
Best Local Similarity 82.0%; Pred. No. 2.4e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 104; Gaps
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/gene="chiA"
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Genetics 167 (3), 1331-1340 (2004)
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join(24. .456,552. .955)
/gene="chiA"
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/gene="chiA"
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complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 CTACACCCGGAGCGCGTTCCTCGAGGCCATCGCCGCGTACCCGGGCTTCGCGCATGGCGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 CGGCGGCGGCGGCGGAGGCGGAGGCAGTGGCGAGCGTGCGAACGTGGCTAACGTGGCTCAC 271
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Pred. No. 2.4e-62;
0; Mismatches 51; Indels 104; Gaps
                                                                        /sub_species="parviglumis"
/db_xref="taxon:76912"
<1. .>1094
/gene="chiA"
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|gene="chiA"
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mol_type="genomic DNA"
cultivar="M063"
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                                                     isolate="p13
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Best Local Similarity 82.0°
Matches 707; Conservative
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       genes in the
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1118;
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                                                         organism="Zea mays subsp. parviglumis"
|mol_type="genomic DNA"
|cultivar="P1331788"
        chitinase
                                                                                                                                                                                                                                                                                                                                                                                                              71.2%; Score 550.8; DB 8;
.larity 81.9%; Pred. No. 3.9e-62;
Conservative 0; Mismatches 52;
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                                                                                                                                                                          /sub_species="parviglumis"
/db_xref="taxon:76912"
                                                                                                                                                                                                                   join(<24. .459,555. .>958)
/gene="chiA"
         evolutionary histories
          Comparative evolutionary histories
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
                                                                                                                                                                                                                                                       join(24. .459,555. .958)
/gene="chiA"
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/product="chitinase"
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/gene="chiA"
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Zea mays subsp. parviglumis isolate p6 chitinase (chiA) gene, complete cds.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of 11445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Zea diploperennis isolate d4 chitinase (chiA) gene,
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Genetics 167 (3), 1331-1340 (2004)
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/organism="Zea diploperennis"
/mol type="genomic DNA"
/cultivar="2317"
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/gene="chiA"
/gene="chiA"
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/product="chitinase"</pre>
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/db_xref="taxon:4576"
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JOURNAL
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 1110)
                                                                                                                                                                                                                                                       Comparative evolutionary histories of chitinase genes in the genus
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Zea diploperennis isolate d3 chitinase (chiA) gene, complete cds.
AY532783
AY532783.1 GI:48093347
                                                                                                                                                                                                                                                                                                                                            Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Pred. No. 7.9e-62;
0; Mismatches 51;
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/organism="Zea diploperennis"
/mol type="genomic DNA"
/culTivar="10003"
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Genetics 167 (3), 1331-1340 (2004)
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/broduct="chitinase
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Sea diploperennis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1110)
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Direct Submission
Direct Submission
Submitted (23-JAM-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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(chiA) gene,
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/mol type="genomic DNA"
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                                                                             /product="chitinase"
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/brotein_id="AAT40053.1"
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|oin(24. .450,550. .953)
|gene="chiA"
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WANNVHRVMPQGFGATIRAINGALECNGNNPAQMNARVGYYKQYCQQLRVDFGPNLTC
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81.6%; Pred. No. 7.9e-62;
iive 0; Mismatches 51;
                                                                                                       /product "chitinase"
join (24. 450,550. 953)
goin (24. 450,550. 953)
goodon_start=1
product="chitinase"
protote:="chitinase"
protote:="chitinase"
for xref="G1:48093354"
/mol_type="genomic_DNA"
/cultivar="P1462368"
/isolate="d6"
                                         /db_xref="taxon:4576"
                                                               /gene="chiA"
join(<24. .450,550.
/gene="chiA"
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Sea diploperennis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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    CGACGCGTTCTTCAACGCCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTT
                                                        cracaccesascecerrecrascececercaasceraeceaecerreseceaecerresece
                                                                                   ----ATTTCTGCTACATCAG
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REFERENCE
AUTHORS
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JOURNAL
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VERSION
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TITLE
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## Sequence 1, Application US/09522714

| Sequence 1, Application US/09522714
| Patent No. 6563020
| GENERAL INFORMATION:
| APPLICANT: Simmons, Carl R. |
| APPLICANT: Simmons, Carl R. |
| TITLE OF INVENTION: Maize Chitinases and Their Use in TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants |
| TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants |
| TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants |
| TITLE OF INVENTION WUMBER: US/09/522,714 |
| CURRENT APPLICATION NUMBER: 60/125,915 |
| EARLIER PILLING DATE: 1999-03-24 |
| NUMBER OF SEQ ID NOS: 32 |
| SEQ ID NO 1 |
| LENGTH: 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
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Gaps:
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US-09-350-600-37

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US-09-522-714-39

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US-08-475-427-15

US-08-475-427-15

US-08-475-427-15

US-08-229-050-10

US-08-229-050-10

US-08-229-050-10

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US-08-229-050-10

US-08-229-05-10

US-08-239-05-10

US-08-08-372-10

US-08-448-398-6

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-DBV TIMEOUT=120 -WARN TINEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPOR=17 -YGAPOP=10 -YGAPEXT=0.5 -DELORY=7
                                                                                                                                             May 23, 2005, 17:19:13 ; Search time 129.26 Seconds (without alignments) 3253.303 Million cell updates/sec
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11. /cgn2_6/ptodatcal/ina/SA_COMB.seq:*
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6: /cgn2_6/ptodatcal/ina/backfiles1.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     nucleic search, using frame plus p2n model
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US-08-449-043-37
US-08-456-265A-37
US-08-455-246-37
US-08-455-244-37
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US-08-457-364-37
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Maximum Match 100%
Listing first 45 summaries
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Match
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GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22

US-10-692-367-12 (1-257) x US-09-522-714-1 (1-1094)

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1297.5 861.5 861.5 825.5 825.5 825.5 825.5 825.5 825.5 825.5

126487437111

Result

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123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
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                                                                                                                                                                                                                                                                                                                                                         103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                                                                                                                                                                                                                                                                  261 CCGGCCTTCTTCGACGCGCTCCTCGCGAGGCCGACGCCTCGTGCGAGGCCAACGGCTTC 320
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Patent No. 5614395
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
                                        1.79e-77
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 ; LOCATION: (42)...(854)
US-09-522-714-21
                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                270 AGTGGCGGC-------GGTGGTGCGAACGTGCGTAGCGTCGTCACC 308
                                                                                                                                                              TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
                                                                                                                                                                           TACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGG 428
                                                                                                                                                                                                                                                                                           ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln1leSer 162
                                                                                                                                                                                                                                                                                                       GGCAGGGTGGCGCGGGGGCGGTGGTGGTGGCGTCAGGCGGCGCTCTGGTTCTGGTTCTAAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               788
                                                                                                                                                                                                         SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
                                                                           62
                                                                                                                      82
                                                                                                                               309 GGCTCCTTCTTCAACGGCATCAAGAGCCAGGCCGGGAGCGGGGGGGAGGAGCAACTTC
                                                                                                                                                                                                                   GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC
                                                      GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr
                                                                                                                     63 AspalaphePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORMATION:
APPLICANT: Simmone, Carl R.
APPLICANT: Simmone, Carl R.
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants;
FILE REPERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT PILING DATE: 2000-03-10
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          849 TACTGCCGCCAGCTCGGCGTCGACCCCGGGCCCAACCTCACCTGC
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Patent No. 6563020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Zea maye FEATURE: NAME/KEY: CDS
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US-09-522-714-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACATTTCTGCTACATAGAAGAGTTAACGGAGCAACACGTAACTACTGCCAGAGCAGC 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrileArgAlaileAsnGly 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGly 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr
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                                                                                                                                                                                                                                                                                  1079
146
33
60
17
                                        NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 5-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-869
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                            US-10-692-367-12 (1-257) x US-08-181-271A-37 (1-1079)
US 08/045,957
                                                                                                                                                                                                                                                                                    7.89e-74
825.50
69.92%
57.03%
56.85%
            FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER:
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Best Local Similarity:
                                                                                                                                                                                                          TOPOLOGY: 11 MOLECULE TYPE:
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Query Match
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108 ---atggaatgtaacggtggtaattccggtgcagtcaacgcaaggattggatactataga 764
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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                           242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                 765 gacriarrichgacacacricerererecerecereceraacerraerree 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALGABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRATING SYSTEM:
COMPATING SYSTEM:
COMPATING SYSTEM:
COMPACTION NUMBER:
PILING DATE: 24-MAY-1995
CLASSIPICATION NUMBER: W6/08/449,315
FILING DATE: 3-JAN-94
FILING DATE: 13-JAN-94
FILING DATE: 13-JAN-94
FILING DATE: 16-JUL-1993
PRICATION NUMBER: W5 07/937,197
FILING DATE: 6-MOY-1992
FILING DATE: 1-MAN-1992
FILING DATE: 1-MR-1991
FILING DATE: 6-FEB-1989
FILING DATE: 6-FEB-1989
FILING DATE: 8-MAR-1988
FILING DATE: 8-MAR-1988
FILING DATE: 8-MAR-1988
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PRIOR DATE:

APPLICATION NUMBER: US 08/042,847

PILING DATE: 6-APR-1993

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION NUMBER: US 07/425,504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                                                                                               Alexander, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                           US-08-449-315-37; Sequence 37, Application US/08449315; Patent No. 5650505
                                                                                                                                                                                                                                                                                                                                                                                                             Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr
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146
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                                                  PRIOR PAPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/768,122

PRIOR APPLICATION NUMBER: US 07/768,122

PRIOR APPLICATION NUMBER: US 07/580,431

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/580,431

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

PRIOR APPLICATION NUMBER: US 07/329,018

PRIOR APPLICATION NUMBER: US 08/045,957

PRIOR APPLICATION NUMBER: US 08/045,957

PRIOR APPLICATION NUMBER: S-1982

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: S-19825/PI/CGC 1727

TELECHOMINICATION INFORMATION:

TELECHONE: (919)541-8614

TELECHONE: (919)541-8614

TELECHONE: (919)541-8614

TELECHONE: (919)541-8614

TELECHONE: (919)541-8614

TELECHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-692-367-12 (1-257) x US-08-449-315-37 (1-1079)
                    JMBER: US 07/848,506
6-MAR-1992
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825.50
69.92%
57.03%
56.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1079 base pairs
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 6-MAR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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Query Match:
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142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
                468 AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTCGGTCGTGGTCCGACCAACTA 527
                                                                SerirpAsniyrAsniyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                          AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
                                                                                                                                                                                                                                                                          708 ---ATGGAATGTAACGGTGGTAATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGA
                                                                                                                           182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet
                                                                                                                                                                                                                      AATAGCGTAAGGCCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                    242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                                                                                                                                                                                         765 GACTATTGTGGACAGCTTGGTGTGGACCCTGGTCCTAACCTTAGTTGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-UUL-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duesing, John H.
Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08444803
Patent No. 5654414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ryals, John A.
Alexander, Danny C.
Beck, James J.
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US-08-444-803-37
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APPLICANT:
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APPLICANT:
APPLICANT:
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43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGly 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGA----
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-692-367-12 (1-257) x US-08-444-803-37 (1-1079)
PRIOR AFFLICATION DATA:

PRELICATION NUMBER: US 07/678,378
FILING DATE: 1-ARE-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 2-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 2-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1933
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825.50
69.92*
57.03*
56.85*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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MEDIUM TYRE: TA LOPPY LIAR COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: PC-DOS/MS-DOS SOFTWARE: Petcher In Release #1.0, Version #1.25 CURRENT APPLICATION DATA: RELEASIPICATION DATA: APPLICATION NUMBER: US/08/449,043 FILING DATE: 13-JAN-94

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION NUMBER: US 07/937,197

FILING DATE: 16-JUL-1993

PRIOR APPLICATION NUMBER: US 07/678,378

FILING DATE: 6-FEB-1991

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 6-FEB-1993

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/165,667

FILING DATE: 6-FEB-1999

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/165,667

FILING DATE: 6-APR-1999

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/165,607

FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/68,122

PRIOR APPLICATION NUMBER: US 07/68,122

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580,431

FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/580,431

FILING DATE: 27-SEP-1999

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/580,431

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580,431

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA: US 09/045,957

FILING DATE: 17-MAR-1999
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PRIOR DATE: 10-00-1593

PRIOR DATE: 10-00-1593

FILING DATE: 6-NOV-1992

PRIOR APPLICATION NUMBER: US 07/678,378

PRIOR APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APPL-1991

PRIOR APPLICATION NUMBER: US 07/676,66

FILING DATE: 6-FEB-1989

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APPL-1993

PRIOR APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-0CT 1989
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APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
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TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 3'
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
            Tarrytown
New York
Y: USA
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                                                                                                                                                                                 240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGGGGGGAAAGATTC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||| :::|||::: ||| 300 TACACCCGGGACTTTCCCCAACTTTGCCAATTCTGTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 ACC------AGACGTGAAATTGCTACCATGTTTGCTCATTTCACTCACGAGACC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrileArgAlaileAsnGly 221
                                                                                                                                                       GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                       23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGly 42
                                                                                                                                                                                                                                                                                                                                                 43 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValYalThr 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe
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Patent No. 5767369

GENERAL INFORMATION:
APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CIEA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 GlnTyrCygArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCyg 257
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520 White Plains Road, P.O. Box 2005
                                                                                                            US-10-692-367-12 (1-257) x US-08-449-043-37 (1-1079)
            Mismatches:
Indels:
          57.03%
56.85%
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-456-265A-37
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
COUNTRY: USA
ZIP: 10591
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-AAY-95
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APPLICANT: Mains, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary Bar
APPLICANT: Moyer, Jean-Marc
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Sherica C.
TITLE OF INVENTION: DAM, SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-AN-94
APPLICATION NUMBER: 08/181,271
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRILING DATE: 6-FEB-1989
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRICK APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/825,504
FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION THE APPLICATION DATA:
                                                                                                                                                                                                                                            STREET: 7 Skyline Drive CITY: Hawthorne STREET Programme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATE: US 07/678,378
APPLICATION NUMBER: US 07/678,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/305,566 FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US 07/368,672
20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
Goodman, Robert M.
               Harms, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 7-SEP-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           USA
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                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||||||| :::||||::: ||| 310 TACACCCGTGACTTTCCCCAACTTTGCCAATTCTGTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ACC------AGACGTGAAATTCTACCATGTTTGCTCATTTCACTCACGAGACC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
                                                                                                                                                                                               GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                   23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGly 42
                                                                                                                                                                                                                                                                                                                                                                                                               63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 GACTATIGIGGACAGCTIGGIGIGGACCCIGGICCTAACCTIAGTIGC 812
                                                                                                                                                                                                                                                                                           153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGA----
                                   1079
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                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                             US-10-692-367-12 (1-257) x US-08-456-265A-37 (1-1079)
                                       Length:
                                                                                                                             Gaps:
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Patent No. 2777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
                                       7.89e-74
                                                      825.50
69.92%
57.03%
56.85%
                                                                       Percent Similarity:
Best Local Similarity:
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APPLICANT:
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                      Alignment Scores:
Pred. No.:
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US-08-455-416-37
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APPLICANT: Mells, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Moye, Alice
APPLICANT: Moye, Jean-Marc
APPLICANT: Sperison, Jean-Marc
APPLICANT: Sperison, Jeffrey B.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Wines, Scott J.
APPLICANT: Williams, Sherica C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                      242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                  GACTATTGTGGACAGCTTGGTGTGGACCCTGGTCCTAACCTTAGTTGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
RATCR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/305,566 PILING DATE: 6-FEB-1989
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FILING DATE: 21-DEC-1990
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APPLICATION NUMBER: US 07/425,504
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                                                                                                                                                                                                                                                              Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                   ; Sequence 37, Application US/08455244
; Patent No. 5789214
                                                                                                                                                                                                                   Alexander, Danny C.
Beck, James J.
Duesing, John H.
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648 AATAGCGTAAGGCCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
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146
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFENCE/DOCKET NUMBER: 36,129
REPENCE/DOCKET NUMBER: 36,129
INFORMATION FOR SEQ 1D NO: 37:
SEQUENCE CHARACTERISTSICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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69.92%
57.03%
56.85%
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TCATGGAACTACAACTACGGAGCGTGTGGTCAAAGTCTCGGTCTTGACCTTTCTACGCCAG 587
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648 AATAGCGTAAGGCCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA 707
142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
                                                                                SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                                                                                    202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
                                                                                                                                                                                                                                                                                                                                       222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArg 241
                                                                                                                                                                                                                                                                                                                                                             ---ATGGAATGTAACGGTGGTGATCCGGTGCAGTCAACGCAAGGATTGGATACTATAGA 764
                                                                                                                                                                 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet
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APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-3AN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UL-1993
PRIOR APPLICATION DATE: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 37, Application US/08454876
; Patent No. 5804693
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
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Neuhaus, Jean-Marc
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STATE: New York
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146
33
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             PRIOR PAPLICATION DATA:

APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-5EP-1990
PRIOR APPLICATION DATA: US 07/368,672
FILING DATE: 0-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA: RAPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
REGISTRATION NUMBER: S-129
REGISTRATION NUMBER: S-129
REGISTRATION NUMBER: S-129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMMUNICATION INFORMATION:
MAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECHONE NUMBER: S-19825/PI/CGC 1727
TELECHONE NUMBER: S-19825/PI/CGC 1727
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-692-367-12 (1-257) x US-08-455-244-37 (1-1079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1079 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825.50
69.92%
57.03%
56.85%
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Best Local Similarity:
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647
                                   240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAAGATTC 299
                                                                                            83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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648 AATAGCGTAAGGCCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA
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             63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765 GACTATTGTGGACAGCTTGGTGTGGACCCTAGTTGC 812
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Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
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; Patent No. 5847258
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
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Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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STREET: 7 Skyline Drive
CITY: Hawthorne
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION UNDERS: US 07/678,378
PRING DATE: 1-APR-1991
PRIOR APPLICATION UNDERS: US 07/305,566
PRING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
PILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/62,847
PILING DATE: 8-MAR-1998
PRIOR APPLICATION NUMBER: US 07/632,441
PILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
PILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/85,504
PILING DATE: 27-SEP-1990
PRIOR APPLICATION NUMBER: US 07/68,122
PRIOR APPLICATION NUMBER: US 07/68,122
PRIOR APPLICATION NUMBER: US 07/768,122
PRIOR APPLICATION NUMBER: US 07/569,431
PPLICATION NUMBER: US 07/569,431
PPLICATION NUMBER: US 07/569,431
PPLICATION NUMBER: US 07/329,018
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Matches:
Conservative:
Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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69.92%
57.03%
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Query Match:
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300 TACACCCGTGACTCTTTCGTTAACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTT 359 468 AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTA 527 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181 647 221 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241 240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAGATTC 299 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161 201 707 360 ACC------AGACGTGAAATTGCTACCATGTTTGCTCATTTCACTCACGAGACC 407 528 rcanggaacnacaacnacgaggaggaggaggagagagagacaggagagaggag 587 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 43 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGlyGly 242 GlnTyrCygArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCyg 257 765 gacrarriergackágerriegrerágaceeregereerkacerragriee 812 US-10-692-367-12 (1-257) x US-08-457-364-37 (1-1079) Mismatches: Indels: Gaps: Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice ; Sequence 37, Application US/08456262 Alexander, Danny C. Beck, James J. Duesing, John H. 57.03% 56.85% Ryals, John A Moyer, Mary B ; Patent No. 5851766 ; GENERAL INFORMATION: ; APPLICANT: Ryals, Best Local Similarity: APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: RESULT 12 US-08-456-262-37 195 162 Query Match: DB: 용 셤 8 요 ò 유 ద ò 임 ò 셤 ð 셤 ò 셤 ሯ 셤 à ò à Š 8

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APPLICANT: Payne, George B.
APPLICANT: Sperison, Jeffrey B.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Utnes, Scott J.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
APPLICANT: WILLIAMS Shericca C.
APPLICANT: WILLIAMS SHERICAN C.
APPLICANT: WILLIAMS SHERICAN C.
APPLICANT: WILLIAMS SHERICAN CORRESPONDENCE ADDRESS:
APPLICANT: APPLICANT C.
APPLICANT: SPECIAL STREET C.
APP
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIPICATION NUMBER: US/08/093,301
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US/08/093,301
FILING DATE: 16-JUL-1993
PRICE APPLICATION NUMBER: US/093,301
FILING DATE: 16-JUL-1993
PRICE APPLICATION NUMBER: US/093,301
FILING DATE: 1-PR-1991
PRICE APPLICATION NUMBER: US/07/092,566
FILING DATE: 1-PR-1991
PRICE APPLICATION NUMBER: US/07/05,566
FILING DATE: 6-PR-1991
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/07/05,667
FILING DATE: 6-PR-1993
PRICE APPLICATION DATA: APPLICATION NUMBER: US/07/05,667
FILING DATE: 1-DEC-1990
FILING DATE: 1-DEC-1990
FILING DATE: 21-DEC-1990
FILING DATE: 20-OCT 1989
FILING DATE: 20-OCT 1980
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FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
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FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,129
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ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
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TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHi8GlyGly 102
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Matches:
Conservative:
Mismatches:
Indels:
S-19825/P1/CGC 1727
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      TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: DNA
US-08-456-262-37
REFERENCE/DOCKET NUMBER:
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69.92%
57.03%
56.85%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: MOYEr, March B.
APPLICANT: Neuhaus, Jean-Marc APPLICANT: Neuhaus, Jean-Marc APPLICANT: Sperison, Christoph APPLICANT: Sperison, Christoph APPLICANT: Stinson, Jeffrey R. APPLICANT: Ward, Eric R. APPLICANT: Ward, Eric R. APPLICANT: Ward, Eric R. TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 166 CORRESPONDENCE ADDRESS:
765 GACTATTGTGGACAGCTTGGTGTGGACCCTGGTCCTAACCTTAGTTGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
SUCTANTE: Batentin Release #1.0, Version #1.25
SUCTANTE: BATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-FEB-1989
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 08/042,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                              Sequence 37, Application US/08456240 Patent No. 5856154 GENERAL INFORMATION: APPLICANT: Ryals, John A.
                                                                                                                                                    Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Griddrich, Leslie B.
Goodman, Robert M.
                                                                                                                                                                                                                                                                                     Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 7
                                                                -08-456-240-37
                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 caaggrircitiaacaaratrarcaaccaagcregraarggrigcgcggggaaagarrc 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 LysArgGinTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGly 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 ACC------AGACGTGAATTGCTACCATGTTTGCTCATTTCACTCACGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr
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PRILING APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-UN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAMM: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFACOM CARRACTERISTICS:

SEQUENCE CHARACTERISTICS:

FORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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Matches:
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MBER: US 07/768,122
27-SEP-1991
                                                                 US 07/580,431
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825.50
69.92%
57.03%
56.85%
                         FILING DATE: 27-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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EDNESS: single
    APPLICATION NUMBER:
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Best Local Similarity:
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MOLECULE TYPE:
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202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
                                                                                                                                                  648 AATAGGGTAAGGCCGGTTCTGAACCGTTTTGGAGCCACCATTAGAGGCTATTAGAGGA 707
                                                                                                                                                                                                   ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
                                                                                                                                                                                                                                                                                                 765 GACTATTGTGGACAGCTTGGTGTGGACCCTGGTCCTAACCTTAGTTGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: 105/08/455,736 FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/093,301
FILING DATE: 13-0AN-1994
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nethaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Vfnes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08455736
Patent No. 5880328
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY CORSTREET: 7 SKyline Drive CITY: Hawthorne STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                         US-08-455-736-37
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APPLICANT:
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240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGAAAAGATTC 299
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Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8619
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-692-367-12 (1-257) x US-08-455-736-37 (1-1079)
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PELLING DATE: 6-FEB-1989

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE: 8-WAR-1988

PRIOR APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

PRIOR APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/68,122

FILING DATE: 7-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 12-APR-1983

ATORNEY/AGENT INFORMATION:

NAME: ELIMET: JAMES SCOCT

REGISTRATION NUMBER: US 07/329,018

FILING DATE: 12-APR-1983

ATORNEY/AGENT INFORMATION:

NAME: ELIMET: JAMES SCOCT

REGISTRATION NUMBER: US 07/329,018

PRIOR NUMBER: US 07/329,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.89e-74
825.50
69.92%
57.03%
56.85%
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STRANDEDNESS: single
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Best Local Similarity:
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3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGly 42
                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
FRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
FRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 8-MAR-1988
FRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 1-DEC-1990
FRIOR APPLICATION NUMBER: US 07/632,441
FRIOR APPLICATION NUMBER: US 07/632,441
FRIUNG DATE: 20-OCT 1989
FRIOR APPLICATION NUMBER: US 07/88,504
FRIOR APPLICATION NUMBER: US 07/88,504
FRIOR APPLICATION NUMBER: US 07/88,122
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FRIUNG DATE: 12-AFR-1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: S-19825/FI/CGC 1727/DIVS/CONT
TELEGRAM: (919)541-8689
THOORNATION TO NOT TO NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1079
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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69.92%
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
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Best Local Similarity:
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                                                                                                                    FILING DATE:
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    TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
                              103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                                                                                            360 ACC------AGACGTGAAATTGCTACCATGTTTGCTCATTTCACTCAGAGACC 407
                                                                                                                                                             GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
                                                                                                                                                                                                                                       142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
                                                                                                                                                                                                                                                                                                                  SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
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Fatent No. 5942662
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Friedrich, Leslie
APPLICANT: Friedrich, Leslie
APPLICANT: Ward, Scott
APPLICANT: Ward, Eric
TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5942662artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: No. 5942662artis Corporation
STREET: 3054 Corrwallis Road, P.O. Box 12257
STATE: NC
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APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-07N-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/971,217
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CLASSIFICATION: 800
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 SMQNCGCQPNVCCSKFGYCG.....GYYRQYCRQLGVDPGNNLTC 257
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                                                                                                                           Sequence:
                              Run on:
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11390874 : ... : "N Total number of hits satisfying chosen parameters:

5695437 seqs, 3066160638 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TTRANS=human40.cdi -LIST=45 -DOCALTGN=200 -THR_SCORE=pct -THR_NAX=100
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Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	11 agraina	equence 11,	equence 29,	equence 33,	equence 29,	equence 33,	equence 71,	equence 59,	equence 45,	equence 45,	equence 65,	equence 65,	equence 61,	equence 47,	equence 47,	equence 73,	equence 63,	equence 23,	equence 37,	equence 23,	equence 67,	equence 4	equence 43,	equence 39,	equence 39,	equence 75,	ednence	equence 25,	equence 762,	equence 3048	equence 13	equence 7,	equence 51	equence 51	equence 69	Sequence 41, Appl Sequence 41, Appl	equence 3															
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                            Variant sequence produced by shuffling techniques r2C2 nucleic acid
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US-10-692-367-11
Sequence 11, Application US/10692367
; Publication No. US20050050595A1
                                                                            1.17e-166
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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
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US-10-389-432B-11
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Query Match:
                                                                    Alignment Scores:
Pred. No.:
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APPLICANT: MILIEY, Mathias L.
APPLICANT: MILIEY, Mathias L.
APPLICANT: Miller, Mathias L.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Activity
FILE REFERENCE: 549162000320,
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 10/389,432
PRIOR FILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-06
PRIOR PLING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-07
PRIOR
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DB:
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; LOCATION: (1)
US-10-692-367-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/10389432B

Sequence 33, Application US/10389432B

Publication No. US20040250309A1

GENERAL INVORMATION:

APPLICANT: Muller, Mathias

APPLICANT: Simmons, Carl

APPLICANT: True, Thom

APPLICANT: True, Thom

TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE

TITLE OF INVENTION: ACTIVITY

FILE REFERENCE: 48942200300

CURRENT APPLICATION NUMBER: US/10/389,432B

CURRENT APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 66

SOFTWARE PARESE PARESEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 771
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Best Local Similarity:
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ORGANISM: Unknown
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  Variant sequence produced by shuffling techniques rl AD4 nucleic acid
                                                                                                                                                                                                                                                                                                                           RESULT 3
US-10-389-432B-29
| Sequence 29, Application US/10389432B
| Sequence 29, Application US/10389432B
| Publication No. US20040250309A1
| GENERAL INFORMATION:
| APPLICANT: Muller, Mathias
| APPLICANT: Thue, Thom
| APPLICANT: True, Thom
| APPLICANT: Talpani, Nasser
| TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
| TITLE OF INVENTION: ACTIVITY
| FILE REFERENCE: 489492000300
| CURRENT FILING DATE: 2003-03-14
| PRIOR FILING DATE: 2001-11-07
| PRIOR PRICATION NUMBER: 60/337,029
| PRIOR FILING DATE: 2001-11-07
| NUMBER OF SEQ ID NOS: 66
| SEQ ID NO 29
| LENGTH: 771
| TYPE: DNA
| ORGANISM: Unknown
| REATURE: COMMENT OF TREE 
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US-10-389-432B-29
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Matches:
Conservative:
Mismatches:
Indels:
                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATNISE:
OTHER INFORMATION: Variant sequence produced by
                                                                                                                                                                                                                                                                           US-10-692-367-12 (1-257) x US-10-692-367-29 (1-774)
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 774
                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                     1.37e-164
1435.00
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Best Local Similarity:
                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)
US-10-692-367-29
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                                                                                                                                                                AACTTCTACACCCGGAGCGCGTTCCTCGAGGCCATCGCCGCATACCACCGGGCTTCGCGCAT
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               TCGATGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGG
                                                 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly
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; Publication No. US2005005058A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: activity
TITLE OF INVENTION: activity
FILE REPRENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
; PRIOR PILING DATE: 2003-10-24
; PRIOR FILING DATE: 2003-14
; PRIOR FILING DATE: 2003-11-06
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR RILING DATE: 2001-11-07
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2001-11-07
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US-10-692-367-29
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                                                        ThriysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln
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APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: World Compositions with chitinase
TITLE OF INVENTION: Activity
FILE OF INVENTION: Activity
FILE REPERRICE: 54916,2000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT APPLICATION NUMBER: 10/389,432
PRIOR APPLICATION NUMBER: 10/389,432
PRIOR PILING DATE: 2003-11-06
PRIOR PILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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; LOCATION: (1)
US-10-692-367-71
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US-10-692-37-33

Sequence 33, Application US/10692367

Publication No. US20050050531

Sequence 33, Application US/10692367

Sublication No. US20050050531

Sublication No. US20050050531

APPLICANT: Mathias L.

APPLICANT: Simmons Carl R.

FILE OF INVENTION: Novel compositions with chitinase TITLE OF INVENTION: activity Y.

FILE REFERENCE: 549162000320

CURRENT FILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-11-06

PRIOR FILING DATE: 2002-11-06

PRIOR FILING DATE: 2002-11-07

PRIOR PLING DATE: 2002-11-07

PRIOR PLING DATE: 2001-11-07

PRIOR FILING DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 84

SOUTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 33
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ORGANISM: Artificial Sequence
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US-10-389-432B-59
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                                                       ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly
                                                                                                                                    GlyGlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnVal
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Publication No. US20040250309A1
GENERAL INFORMATION:
APPLICANT: Mathias
APPLICANT: Simmons, Carl
APPLICANT: True, Thom
APPLICANT: Simmons, Carl
FILE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
FILE REFERENCE: 4894922000300
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 59
SEQ ID NO 59
LENGTH: 768
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TYPE: DNA
ORGANISM: Unknown
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US-10-389-432B-59
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ABRPHGTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100
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                                                                     ATGAACAACGTGCACGTGTGATGCCGCAGGGCTTTCGGCGCCCACCATCAGGGCCATCAAC
                                                                                                                                                                                                                                                                                                        61 ACGACCGACGACTACTGCGGCGACGGGTGCCGGTCGGGCCCGTGCCGCTCGGGCGGTT
                     178 ATCTCGTGGAACTACAACTACGGGCCCGCGGGGAGGGCCCATCGGCTTCGACGGGCTCGGG
                                                                                                                                                                        201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn
                                                                                                                                                                                                                                                                        221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Variant sequence produced by shuffling techniques OTHER INFORMATION: 4N1/80_F8 nucleic acid
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APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
TITLE OF INVENTION: ACTIVITY
FILE REPERRICE: 489422000300;
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT PILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PLING DATE: 2001-11-07
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 771
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Matches:
Conservative:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Variant sequence produced by shuffling techniques
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TILLE OF INVENTION: Novel compositions with chitinase
TITLE OF INVENTION: Activity
TILLE REPERENCE: 54916200320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT PILING DATE: 2003-10-22
FRIOR APPLICATION NUMBER: 10/389,432
FRIOR APPLICATION NUMBER: 10/290,086
FRIOR FILING DATE: 2002-11-06
FRIOR PELING DATE: 2002-11-07
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR APPLICATION NUMBER: 5004-10-27
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 771
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Matches:
Conservative:
Mismatches:
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94.94%
95.21%
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Best Local Similarity:
Query Match:
DB:
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; NAME/KEY: CDS
; LOCATION: (1).
US-10-692-367-59
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Pred. No.:
Score:
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                                       GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
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          241 AACTICIACACCCGGAGCGCGTICCTGAGCGCCGTCAAGGCGTACCCAGGCTICGCCCAT 300
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US-10-692-367-45

Sequence 45, Application US/10692367

Septicant: Mailer, Mathias L.

APPLICANT: Minchias L.

APPLICANT: True, Thom

APPLICANT: Yalpani, Nasser

ITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: Activity,

FILE REPERENCE: 549162000320

CURRENT FILING DATE: 2003-10-22

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/290,086

PRIOR PILING DATE: 2002-11-06

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 5002-10-22

NUMBER OF SEQ ID NOS: 84

SEQ ID NOS: 84

SEQ ID NO 45
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Matches:
Conservative:
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97.28%
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; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-45
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Pred. No.:
Score:
Percent Similarity:
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Publication No. US20040250309A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Muller, Mathias
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
ITILE OF INVENTION: ACTIVITY
ITILE OF INVENTION: ACTIVITY
FILE REFERENCE: 489492000300
CURRENT FILIAGO DATE: 2003-03-04
CURRENT FILIAGO DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
                                                                             US-10-692-367-12 (1-257) x US-10-692-367-45 (1-774)
  Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 771
                                                                                                                 1.57e-157
1377.00
96.50%
93.39%
94.83%
                                                                      OTHER INFORMATION: OTHER INFORMATION:
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Best Local Similarity:
                                              TYPE: DNA
ORGANISM: Unknown
                                                                                 ; OTHER INFORMAN
US-10-389-432B-65
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                                                    APPLICANT: MILOSCAMILOR METHING L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Wasser
TITLE OF INVENTION: Novel compositions with chitinase
TITLE OF INVENTION: Activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT APPLICATION NUMBER: 10/389,432
PRIOR PILING DATE: 2003-10-22
PRIOR PILING DATE: 2003-11-06
PRIOR FILING DATE: 2002-11-06
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-3
SEQ ID NOS: 84
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 774
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Matches:
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Sequence 65, Application US/10692367; Publication No. US20050050595A1; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)
US-10-692-367-65
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141 ThruysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
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                                                              AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100
                                                                                                                             101 GlyGlySerGluValGluArgLyBArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
                                                                                                                                                                                                                     161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
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ValThraspalaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys
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OTHER INFORMATION: Variant sequence produced by shuffling techniques PERATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 61, Application US/10692367

publication No. US20050050595A1

GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Alabani, Nasser

TITLE OF INVENTION: activity

FILE REPRENCE: 54916200320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-22

PRIOR APPLICATION NUMBER: 10/280,086

PRIOR PILING DATE: 2003-11-06

PRIOR FILING DATE: 2003-11-06

PRIOR FILING DATE: 2001-11-07

PRIOR POWNER: FASTER FOR WINDOWS: 84

SOFTWARE: FASTER FOR WINDOWS: 84

1 FENTANT: 77
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                                                                                                                                                                                                                                                                                                                                   241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
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US-10-389-432B-61
Sequence 61, Application US/10389432B
Sequence 61, Application US/10389432B
Publication No. US20040250309Al
GENERAL INFORMATION:
APPLICANT: Muller, Mathias
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 489492000300
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PLING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Unknown
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Pred. No.:
Score:
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                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                  US-10-692-367-12 (1-257) x US-10-692-367-61 (1-771)
                  4.17e-157
1373.50
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94.59%
             Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
, LOCATION: (1)
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Search completed: May 23, 2005, 22:41:51 Job time : 419.647 secs

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BM73641 952051A06
CA270202 SCGGLB205
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CB981100 CAB70003
CB9811100 CAB70003

Perfect score:

Seguence:

protein

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Run on:

Scoring table:

Total number Minimum DB Maximum DB

Searched:

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Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org, or NCBI, www.ncbi.nlm.nlh.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
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1 (bases 1 to 1179)
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Zea mays PC0155066 mRNA sequence.
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/organism="Zea mays"
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AY103546
LOCUS
DEFINITION
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SOURCE
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BG837653 Zm10_01e1
CD435649 EL01N0364
CO524416 3530_1_16
CN133023 OX1_9_D11
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                                                                                                                          May 23, 2005, 17:04:03 ; Search time 2300.33 Seconds (without alignments) 4252.663 Million cell updates/sec
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                   GenCore version 5.1.6
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/note="vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channeI-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG837479 958 bp mRNA linear BST 25-MAY-2001 Zml0 10h09 A Zml0 AAPC ECORC Fusarium graminearum_corn_silk Zeamays_cDNA clone Zml0_10h09, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 958)
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Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P.,
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A,
Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk
Chamnel Inoculation with Fusarium graminearum
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                       Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KlA 0C6,
869 TACTGCCAGCAGCTCCGCGTCGACCCCAGGGCCCCAACCTCACTTGC 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
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                                                                                    /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                            GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
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Library"
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xref="MaizeDB:638921"
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EAST 25-MAY-2001

ZM10 01610 A ZM10 AAFC ECORC FUBArium graminearum corn_silk Zea

MASS CDNA Clone ZM10_01e10, mRNA sequence.

BG837663.1 GI:14203986
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1 (Dassel 1 to 855)
Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum
 82
aLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGl
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                                                       ySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluTh
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Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Agriculture Experimental Parm, Ottawa, Ontario,
CANADA
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Email: harielj@agr.gc.ca.
Location/Qualifiers
1. .855
/organism="Zea mays"
/mol_type="mRNA"
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Fax: (613) 759-6566
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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morning (~10 am) with I ml of a macroconidial euspension (500, 000 sporess/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel. RNA from five silk channels was pooled."
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/dev_stage="4-5 days post-silk emergence"
/clone_lib="Zm10_AAFC_ECORC_Fusarium_graminearum_corn_silk
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3530_1161_1E12.y 1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
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Invitrogen from multiple tissues"
Invitrogen from multiple tissues"
leaf, root tips, whole seed, embryo; Vector: pCNV-SPORT 6.1; Site_1: EcoRV; Site_2: Not1; Maize Gene Discovery Forject contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement
                                                                                                                                          290 TACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGG 349
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    (bases 1 to 767)

                                                                                                                  123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys
                                                                                                                                                                                                                                                                                                                                                                  143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer
                                                                                                                                                                                                                                  163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIIeGlyPheAspGlyLeuGlyAspPro
                                                                                                                                                                                                                                                                                                           530 recaactacaactaceeecceeedeaaeeeccarceerreaceecreeeecreee
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                                     SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr
                                                             Maize ESTs from various cDNA libraries sequenced at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotyostanford.edu
Plate: 3530 1 161 1 row: E column: 12.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 aleuGluCysAsnGlyAsnAsnProAla 231
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Department of Biological Sciences
Stanford University
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Laide, Banicoldeae; Andropogoneae; Zea.

Laide, Banicoldeae; Andropogoneae; Zea.

Laide, Banicoldeae; Andropogoneae; Zea.

Laide, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome

Comparison to the rice genome

Genome Ree 14 (10), 1932-1937 (2004)

Contact: Lai, Jinsheng

Dr. Joachim Messing's lab

Wakeman Institute, Rutgers University

190 Prelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-5735
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to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20x to 80x reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed, 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 2 dap endosperm and embryo; 12. 17 dap whole seed; 11. 2 dap endosperm and embryo; 12. 17 dap whole seed; 11. 2 dap endosperm and embryo; 12. 17 dap whole seed; 11. 2 dap endosperm and embryo; 12. 17 dap whole seed; 11. 2 dap endosperm and embryo; 13. 14 dap whole seed; 11. 2 dap endosperm and embryo; 13. 14 dap whole seed; 11. 2 dap endosperm and embryo; 13. 14 dap whole seed; 11. 3 dap endosperm and embryo; 13. 14 dap endosperm and embryo; 14. 14 dap endosperm and embryo; 15. 17 dap endosperm and embryo; 15. 14 d

247 AGTGGCGGC------GTGGTGCGAACGTGGCTAGCGTCACC 285 346 TACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGG 405 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspFro 182 127 cagaactigcegereceaeccaaacerarecrecageaagriregeracrecegecaegaec 186 187 dacdadrachecedeceacedereceaercedecederecederecedecedecedecedecede 286 GGCTCCTTCTTCAACGGCATCAAGAGCCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTC 345 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162 GlabanCysGlyCysGlaProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22 23 ABPG1uTyrCyBG1yABpG1yCyBG1nSerG1yProCyBArgSerG1yG1yG1yG1y 42 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82 767 196 9 8 7 Length:
Matches:
Conservative:
Mismatches:
Indels: Gabs: = (1-767)US-10-692-367-12 (1-257) x CO524416 2.38e-99 1110.50 93.18% 89.09% 76.48% Percent Similarity: Best Local Similarity: Alignment Scores: m 103 163 123 43 406 Query Match: DB: Мо.: ORIGIN ò 셤 ò 8 දි දි ò 염 \$ 6 B 셤 ሯ 셤 ò

Locations and recomplete streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

El (bases 1 to 837)
S Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Bastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
Cother ESTS: OX1 9 D11.b1 A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 582 1860 /db xref="taxon:458" / db xref="taxon:4588" / clone="OX1 9 D11 A002" / lb A00 Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
Sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG). CN133023
OX1_9_D11.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor CDNA_clone OX1_9_D11_A002 5', mRNA sequence. 222 765 203 AsnvalHisArgvalMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 646 GGCAGGGTGGCGCGGGACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAAC GlyargvalalaargaspalavalvalalaaheLysalaalaLeuTrpPheTrpMetAsn 837 199 8 27 12 Matches: Conservative: Mismatches: Indels: /organism="Sorghum bicolor" /mol_type="mRNA" /cultivar="BTx623" Sorghum bicolor (sorghum) Sorghum bicolor CN133023.1 GI:45963543 .21e-98 1096.00 84.15% 80.89% 75.48% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: 183 source LOCUS DEFINITION SOURCE ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT REFERENCE AUTHORS RESULT 6 CN133023 FEATURES ORIGIN Score: 셤 셤 ઠે

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Matches:
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Mismatches:
Indels:
         Contract: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
1. 710.
14 (10), 1932-1937 (2004)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 710)

Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F.,

Laifins,B., Becraft,P. and Messing,J.

Characterization of the maize endosperm transcriptome and its

comparison to the rice genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142
                                                                                                                                                                                                                                                                                                                                                                                                                               GlyArgvalalaArgAspAlavalValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697
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                                                                                                                                                                                                                                                       SerGluvalGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
                                                                                                                                                                                                                                                                                                     ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln1leSer 162
                                                                                                                                                                                                                                                                                                                                                                                                        518 AGGCAGTGGCCGTGTGCCGCGGGTCAGAAGTACTACGGGCGCGGCCCGCTGCAAATCTCG 577
                                                                      CAGAACTACGGCTGCCAGGTTACTGCTGCAGCAAGTTCGGTTACTGCGGCACGACC 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GInAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
                                                                                                                                           G1yG1yG1yG1yG1yG1yG1yG1yG1yG1yB1gAsnVa1A1aAsnVa1Va1Thr
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//note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site 1: BCORV, Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO520138 716 bp mRNA linear EST 15-JUL-: 3530 1 132 1 F10.y 1 3530 - Full length cDNA library created by Invitrogen From multiple tissues Zea mays cDNA, mRNA sequence.
                                                                     GATCAGATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCCTACTGCGACGCAGCA
                                                                                                                  142 ysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleS
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                                                   ----His-PheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrL
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                 GCATGCAGGACCTTTGATCTGACCGACCGATCGTCGTCGTCATGCTGACCATGCATTTTC
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Maize ESTs from various cDNA libraries sequenced at
University
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/mol type="mRNA"
/cultivar="B73"
/db xref="taxon:4577"
/tisue_type="multiple"
/dev stage="varies by tissue"
/lab_host="DH108"
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Contact: Walbot V
Department of Biological Sciences
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OG3CW08TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0778B15, v genomic survey sequence.
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clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                           Taday, C. Tannordae, Muliphogomeae; Sea.

(Dases I to 978)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citck, R.W., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Char GSSs: OG3CW08TH

Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea maye"
/mol type="qenomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:4577"
/clone="zwhEMa0778B15"
/clone="zwhEMa0778B15"
/note="zw-Vector: pBGSEr, Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Faxi: 301-81-elaw@tigr.org
Seq pilimer: TF
Class: sheared ends.
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is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleutrone; 4 immature tassels, stages from 12 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 ady old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (http://www.genome.arizona.edu/orders). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."
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DRIGIN

ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142 417 Accepcicicades de caracterantes de contratos de contr 117 chgaacrigcigcrigccaaactrcrigcrigcaagriccactacrigcigcacaaaaa 176 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22 TACACCCGGAGCGCGTTCCTGAGCGCCGTCAACGCGTACCCGGGCTTCGCCCATGGCGGG SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr GACGCGTTCTTCAACGCATCAAGAACCAGGCCGGGAGCCGGGTGCGAGGAGCTTC 716 180 7 13 Length:
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Conservative:
Mismatches:
Indels: Gaps: US-10-692-367-12 (1-257) x CO520138 (1-716) 7.72e-91 1024.00 93.50% 90.00% Percent Similarity: Best Local Similarity: Scores: m 63 297 83 357 103 123 143 163 Query Match: Alignment S Pred. No.: 셤 g ò ద ò g ò 쉱 ò 셤 ò g à 셤 8 ઠ

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/clone_lib="ADI"
/note="Organ: seedlings inoculated with Gluconacetobacter diazotroficans; Vector: pSportl; Site_l: Sall; Site_2: Mot!; An unidirectional cDNA library generated from fleedlings inoculated with Gluconacetobacter diazotroficans]. CDNA was prepared from polyA+ mENA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                          CA197556 647 bp mRNA linear EST 25-SEP-2003
SCBFRD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11
5', mRNA sequence.
CA197556
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Bukaryota, Vizidiplantea, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Vizidiplantea, Streptophyta, Poales, Poaceae, PACCAD
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                          597 IGGAACTACAACTACGGGCCGCC-GGGAGGACATCGGCTTCAACGGGCTCGCCGACCC 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
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Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Matches:
Conservative:
Mismatches:
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plate: 067 row: A column: 11
Seg primer: 77 Promoter Primer.
Location/Qualifiers
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/db_xref="taxon:4547"
/clone="SCBFAD1067A11"
/lab_host="DH10B"
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                                                                                                                                                             ValAsnLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGly 150
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                                                                               GlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAla 170
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 628)
Walbot,V.
                                  AlaGlnMetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyValAsp 250
----AACGIGGCIAGCGIIGICACCGACGCAIICIICAACGGCAICAAG 107
                      AsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuGlu
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/cultivar="BMS (Black Mexican Sweet)"
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Fax: 650 725 8221
Email: walborostanford.edu
Plate: 952051 row: A column: 06.
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Contact: Walbot V
Department of Biological Sciences
Stanford University
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// notes "Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promegal. cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on positive clones."
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/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
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                                     stationary growth
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/dev_stage="mixed logarithmic and
phases"
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Mismatches:
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xref="taxon:4577"
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/db xref="taxon:4547"
/clone="SCQSLB2051F10"
/lab host="DH10B"
/clone_lib="LB2"
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                                   625 bp mRNA linear EST 11-MAR-2002
- BMS tissue from Walbot Lab (reduced rRNA) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 GluhlallehlahlaTyrProGlyPheAlaHisGlyGlySerGluValGluArgLysArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AGCGCCGTCAACAAGTACCCGGGCTTCGCCCATGGCGGGACGGAGGGGGAGGGGCAAGGGC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 129
                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 625)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="taxon:4577"
/db_xref="taxon:4577"
/tissue f-ype="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
                                                                                                                                                                                                                                           Maize ESTs from various cDNA libraries sequenced at Stanford
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Matches:
Conservative:
Mismatches:
Indels:
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Plate: 952073 row: H column: 05.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="DH10B"
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                                                     952073H05.yl 952 - BMS t.mays cDNA, mRNA sequence
                                                                                                  BM895383.1 GI:19350851
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989.00
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68.11%
                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                        Contact: Walbot V
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COMMENT
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AUTHORS
TITLE
                         BM895383
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SCGSLB2051F10.g LB2 Saccharum officinarum cDNA clone SCQSLB2051F10 CA270202
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Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsn 229
                                                                                                          150 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro 169
                                                                                                                                                                                                                                                                                                                               190 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluvalAsnLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAla 149
                                                   311
                                                                                                                                               170 AlaGiyArgAlalleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 189
                                                                                                                                                                                                                                                    492 CAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAACGGGAACAAC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes "Organ: Lateral buds from plants adult plants growing in greenhouse, Vector: pSportl, Site. 1: Sall; Site. 2: Not1; An unidirectional cDNA library generated from [Lateral buds from plants adult plants growing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
                            Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Pax: 55 19 3788 1089
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Plate: 051 row: F column: 10
Seg primer: T7 Promoter Primer.
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Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

(bases 1 to 801)

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Anfuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.

A Sorghum EST database: mechanically damaged and methyl

REFERENCE

TITLE

Sorghum bicolor (sorghum)

VERSION KEYWORDS SOURCE ORGANISM

Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tal: 706 542 1860
Fax: 706 583 0210

jasmonate-treated leaves
Oubublished (2003)
Other ESTE: WOUND1 75 B02 b1 A002
Contact: Cordonnier-Pratt MM

Tue

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greenhouse]. cDNA was prepared from polyA+ mRNA using SuberScript Plasmid System Kit (Invitrogen). The Gouble-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public...
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Mismatches:
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980.50
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/note="Organ notes of the part of the part
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum bicolor"
/mol type="mkN4"
/uolivar="BTx62"
/db_xref="taxon:4558"
/clone="wOUND1" 75_B02_A002"
/lab host="DH108-Tl phage-resistant E. coli"
/clone_lib="Wounded leaves"
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EST 01-APR-2004

CN151443 101-APR-2 CN151443 1002 Wounded leaves Sorghum bicolor CDNA clone WOUND1_75_B02_A002 5', mRNA sequence.

LOCUS DEFINITION

CN151443

ACCESSION

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Percent Similarity:
Best Local Similarity:
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CAB70003_IaP_C05 Cabernet Sauvignon Berry Post-Veraison - CAB7
Vitis vinifera cDNA clone CAB70003_IaP_C05 5', mRNA sequence.
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermarophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermarophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, Vitaceae, Vitis.
1 (bases 1 to 856)
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
Jones, K. and Cook, D.
                                                                                                                                                              GlyGlySerGluValGluArgLysArgGluIleAlaAla-PhePheAlaHisAlaThrHi 120
|||||||||||||
|GGCGCTCGGAGGACGACGCGAAGCGCGAAGCCGCCCTTCTCGCTCACGCCACA 482
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                                                               GACGCGTTCTTCAACGGCATCAAGAACCAGGCCGGAAGTGGGTGCGAGGGCAGCAACTTC 362
                                                                                                                         TACTCGCGCGACGCGTTCCTGAGCGCTGCCAGTGCCAGTGCGTACTCCGGCTTCGCCCAG 422
                                                                                                                                                                                                                         BGluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPr 140
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GAGCTACACACACGGGGCGGCGCGCGGGGGCAAAAAGTACTACGGAAGAGGCCCCCTGCA 602
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/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
/db_xref="texon:29760"
/clone="CAB70003_laF_C05"
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CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, US
Tel: 530 754 6617
Fax: 530 754 6617
Email: drcook@ucdavis.edu
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/dev stage="Post-Version, 18-19 brix"
/lab_host="DH5alpha"
/lab_host="DH5alpha"
/clone lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
/clone lib="Cabernet Sauvignon Berry Fite l: Sfi1; Site 2:
Sfi1; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8
berries. Samples were collected post-veraison from
field-grown vines during stage III of berry growth at 89
days after full bloom. Berries soluble solid concentration
ranged between 18-19 brix. Sampled vines were located at
the University of California, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and directi
onally cloned. 5'and 3' adaptors were used in cloning as
follows: 5'-AACAGTGGTATCAACGCAGAGTGCATTACGCCGGCGGG-3' and
5'-ATTCTAGAGGCCGACATG-dT(30)NN-3'. Library was
constructed using the Clontech Creator SNART kit and
size-selected to contain the 0.5-3 kb size fraction."
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Search completed: May 23, 2005, 20:41:24 Job time: 2308.33 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: May 23, 2005, 11:14:26 ; Search time 2450.33 Seconds

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14890.544 Million cell updates/sec

Title: US-10-692-367-69

Perfect score: 753
Sequence: 1 tcgatgcagaactgcggctg......ggcccaacctcacttgctga 753

Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 4708233 segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466 Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmbl:*

1: gb_ba:*
2: gb_lrtg:*
3: gb_in:*
4: gb_om:*
5: gb_om:*
7: gb_pat:*
7: gb_ph:*
9: gb_pt:*
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13: gb_om:*
14: gb_om:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 810)

Huynh, O.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.
Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed J. Biol. Chem. 267 (10), 6635-6640 (1992)
                                                                                                                                             GGGCAGAAGTACTACGGGCGGGCCGCTGCAGATCTCGTGGAACTACAACTACGGGCC
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GAGCGCCGTCAAGGCCTACCCAGGCTTCGCCCATGGCGGGCAGGTCGCAGGTGCAGGCGCAAGGC
                                                 CGAGATCGCCGCCTTCTTCGCGCACGCCACGCACGAGACCGGGCCATTTCTGCTACATCAG
                                                                                   CGAGATCAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCCGC
                                                                                                CGAGATCAACAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCGCC
                                                                                                                                GGGCAGAAGTACTACGGCCCCCCCCTGCAGATCTCGTGGAACTACAACTACGGGCC
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) seed DNA.
Location/Qualifiers
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gene, 3'end.
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Zea mays chitinase B (seed chitinase)
M84165
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/organism="Zea mays"
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/db_xref="taxon:4577"
/tissue_type="seed"
/tissue_lib="Lamda GT 10 cc
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/evidemce=experimental
/product="chitinase B"
/protein_id="AAA33445.1"
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CDS

FEATURES

COMMENT

TITLE

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MZECHITA 843 bp DNA linear PLN 27-APR-1993
Zea mays chitinase A (seed chitinase) gene, complete cds.
M84164
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Pred. No. 1.1e-82;
0; Mismatches 28; Indels
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xref="GI:168443"
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llarity 95.9%;
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B.A.
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(chiB) gene,
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (13-JNN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                           CAACGIGCACGGIGTGATGCCGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGC
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                                                                                                           CGGCAGGGTGGCGCGGGGCGCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAA
                                                                                                                                                       caacadegridececadeacecericarcecerricaacaceecercriderricagardaa
                                                                                                                                                                                                    CAACGTGCACCGTGTGATGCCGCAGGGCTTTCGGCGCCACCATCAGGGCCATCAACGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                751
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subsp. parviglumis isolate p15
cds.
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<14. .>976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<14. .449,573. .>976)
/gene="chiB"
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Genetica 167 (3), 1331-1340 (2004)
15280246
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join(14. .449,573. .976)
/gene="chiB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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Tiffin, P.
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Tiffin, P.
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Whyth, O.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.
Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed J. Biol. Chem. 267 (10), 6635-6640 (1992)
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                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                   source text: Zea mays (library: Lamda GT 10 corn
) seed DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="seed"
/tissue_lib="Lamda GT 10 corn seed (imbibed)"
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Pred. No. 5.2e-76;
0; Mismatches 48; Indels 21
                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="seed chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="seed chitinase"
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al Similarity 91.0%;
698; Conservative
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                                                                                                                                                                             CAAGAACCAGGCCGGGAGCGGGTGCCGAGGGAACTTCTACACCCGGAGCGCGTTCCT 245
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                                             GCAGAACTGCGGCTGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAAC
                         Gaps
                      Indels 123;
 Length 1121;
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Score 582.6; DB 8;
Pred. No. 1.3e-68;
0; Mismatches 19;
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 tch 77.4%; al Similarity 83.7%; 727; Conservative
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Best Local S
Matches 727
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1127 bp DNA linear PLN 29-JUL-2004 parviglumis isolate p2 chitinase (chiB) gene,

Zea mays subsp. parvigl complete cds. AY532723 AY532723.1 GI:48093227

AY532723

DEFINITION

ACCESSION VERSION KEYWORDS

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/translation="Makagaprusaaquvtlglsllcavagpaaqucgcqpnvccsk
pgycgttdbycgdgcQsgpcbsggggssgggganvasvytgsppngtsggagggggg
ppytrgqppstayeqbahdGsqvqgkrblatpethethethethethethey
ppytrqppclaguxytggstlg1smynygppgra1gppglggpyrgpyxpayvbraa
lwfwmnsvhgvyrqyrggtattralngaleggnnpaqwnarvgyyrqycgpp
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Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                               genna
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                                                                                                                                                                                                                             Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAACTIGCGGCTGCCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC
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                                                                                                                           the
                                                                                                                        Comparative evolutionary histories of chitinase genes in zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
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                                                                                                                                                                                                                                                                                              1...127
/organism="Zea mays subsp. parviglumis"
/orditivar="genomic DNA"
/cultivar="p134064"
/isolate="p2"
/db_ref="taxon:76912"
<14...>980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.8%; Score 578.6; DB 8;
llarity 83.3%; Pred. No. 4.3e-68;
Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(<14. .449,577. .>980)
/gene="chiB"
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/db_xref="G1:48093228"
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/gene="chiB"
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/product="chitinase"
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Tiffin, P.
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nes 727; Conserv
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
TATTAACCTCGCTCTTCAGCGCGCGCGGGTTCTTTGATTTTTGACCCATCATGCTGATC
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    forganism="Zea diploperennis"
    fmol type="genomic DNA"
    cultivar="P1441932"
    fsolate="d5"

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Genetics 167 (3), 1331-1340 (2004)
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/db_xref="c1:48093260"
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AX532738 1081 bp DNA linear PLN 29-JUL-2004
Zea diploperennis isolate d4 chitinase (chiB) gene, complete cds.
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Genetics 167 (3), 1331-1340 (2004)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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/cultivar="2317"
/isolate="d4"
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Submitted (23-JAN-
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complete cds.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 1081)
Tiffin,P.
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Zea diploperennis isolate d2 chitinase (chiB) gene,
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Pred. No. 1.9e-67;
0; Mismatches 22
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mol type="genomic DNA"
cultivar="9476"
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/gene="chiB"
join(<14. .446,558. .>961)
/gene="chiB"
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/db_xref="GI:48093256"
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join(14. .446,558. .961)
gene="chiB"
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<14. .>961
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              CCCAACCTCACCTGCT 958
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ilarity 84.1%;
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/brotein id="AAT40011.1"
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FYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFFAHATHETCHFCYTSEINKSNAYCD
FYTRSAFLSAVKAYPGGFGATTRAINGALECGGNNPAQMNARVGYYRQYCRQLGVDPGPNL
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                 GATGAACGCGCGCGTCGGCTACTACAGGCAATACTGCCGCCCAGCTCGGCGTCGACCCCCGG
                    CGGCGCCACCAGGGCCATCAACGGCGCCCTCGAGTGCGGCGGCAACAACAACCCCGCCCA
                                                       GATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGTCGACCCAGG
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(chiB) gene,
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Zea diploperennis isolate d8 chitinase
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join(<14. .446,558. .>961)
/gene="chiB"
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Genetics 167 (3), 1331-1340 (2004)
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join(14. .446,558. .961)
/gene="chiB"
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Tiffin, P.
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Pred. No. 1.9e-67;
); Mismatches 22
                                                     . >961)
                                                                                                                                                             /product="chitinase"
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xref="taxon:4576"
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/translation="wakagaprusaaqluticialalicanagaaquoccopnuccsk 
FGYCGTTDEYCGDGCQSGPCRSGGGGGSSGGGGANVASVUTGSFFNGIKNQAGSGCEG 
KNFTRSAFLSAVKAYPGFAHGGSAVQGKRETAAFPHATHETGHPCY ISEINKSNAY 
CDPSKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAFKA 
ALMFWNNSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQYCRQLGVDPGP 
NLTC"
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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTT
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                                                                 parviglumis
                                                                                                                                                                                                                                                                                                                                           Score 572.4; DB 8;
Pred. No. 2.9e-67;
0; Mismatches 21;
                                                                 /organism="Zea mays subsp.
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83.7%;
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les 725; Conservative
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Zea mays subsp. parviglumis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                    CAAGAACCAGGCCGGGAGCGGGGGGGGAAGAACTTCTACACCCGGAGCGCGTTCCT
                                                                                                                                                  GTACTACGGGCGCGCGCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGGAG
                                                 CAAGAACCAGGCCGGGAGCGGGTGCGAGGAGCAAGAACTTCTACACCCGGAGCGCGTTCCT
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Genetics 167 (3), 1331-1340 (2004)
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Tiffin, P.
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Zea mays subsp. parviglumis
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1134)
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                                                            CGTGGTGGCGTTCAAGGCGGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGATGCC
                                                                     766 CGTGGTGGCGTTCAAGGCGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGGTGGTGCC
GGGGCAGAAGTACTACGGGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCC
                                 CGCGGGGAGGCCATCGGCTTCGACGGGTCGGGGACCCCGGCAGGGTGGCGCGGGACGC
                                                                                                   GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGCGAACAA
                                                                                                                                            CCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGT
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                    CGCGGGGAGGGACATCGGCTTCGACGGCTCGGGACCCCCGGCAGGGTGGCGCGGGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                   chitinase genes in
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mol type="genomic DNA"
/cultivar="M063"
                                                                                                                                                                                                                                                                                                                                                                                                  Comparative evolutionary histories of zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_species="parviglumis"
/db_xref="taxon:76912"
<26. .>987
/gene="chiB"
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join(26. .464,584. .987)
/gene="chiB"
                                                                                                                                                                                      CGACCCAGGGCCCAACCTCACTTGCT 751
                                                                                                                                                                                                  CGACCCGGGCCCAACCTCACCTGCT 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolate="p13"
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Tiffin, P.
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1123 bp DNA linear PLN 29-JUL-2004
Zea mays subsp. parviglumis isolate p6 chitinase (chiB) gene,
AY532729
AY532729.1 GI:48093239
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                                            Gaps
                                            122;
Length 1134;
                                         Indels
                                                                                                                                                                                                                                                         CAGCAGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCT
                                         21;
  DB 8;
  Score 570.4; DB 8
Pred. No. 5.3e-67;
0; Mismatches 21;
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VERSION
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1127 bp DNA linear PLN 29-JUL-2004 subsp. parviglumis isolate pl2 chitinase (chiB) gene,
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1 (bases 1 to 1127)
Tiffin, P.
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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              GTCTTCCGCGCGCCGCAGGTTCTTTGATTTTGACCCATCATGCTGATCTATTTT
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                                                                                                               ACATCAGCGAGATCAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGT
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/gene="chiB"
join(<14. .452,579. .>982)
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/db_xref="taxon:76912"
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Genetics 167 (3), 1331-1340 (2004)
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/mol_type="genomic DNA"
/cultivar="M106"
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Zea mays subsp. parviglumis
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Tiffin,P.
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CEGKNFYTRSAFLSAVKAYFGFAHGGSQVQGKREIAAFFAHATHETGHFCYISEINKS
NAYCDFTKRQMPCAAGQKYYGKBFLQISWNYNYGPAGRAIAFHETGHFCYISEINKS
FKAALWFWMNSVHGVYPQGFGATTRAINGALECGGNNPAQMNARVGYYRQYCRQLGVD
PGPNLTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein id="AAT39998.1"
/db xref="GI:48093240"
/translation="MARAKAGAPRVSAPQQLVTLGLALLCAVAGPAAAQNCGCQPNVC
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                                                                                                                                      genus
              Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>CAGCAGTGGCGGCGGTGCTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGG</u>
                                                                                                                                                                                                                                                      University of Minnesota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAAC
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                                                                                                                                    of chitinase genes in the
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                                                                                                                                                                                                                                                                                                                     /organiem="Zea mays subsp. parviglumis"
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/cultivar="P1331788"
                                                                                                                                                                                                                                                                      1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. .1123
                                                                                                                                                                                                                  Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology,
                                                                                                                                                                                                                                                                                                                                                                                         /sub_species="parviglumis"
/db_xref="taxon:76912"
                                                                                                                                    Comparative evolutionary histories
                                                                                                                                                    zea and family poaceae Genetics 167 (3), 1331-1340 (2004)
15280246
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join(<8. .455,580. .>983)
/gene="chiB"
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join(8. .455,580. .983)
/gene="chi8"
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product="chitinase"
                                                                                                                                                                                                                                                                                                                                                                            'isolate="p6"
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larity 83.4%;
Conservative
                                                                                                    (bases 1 to 1123)
                                                                                                                                                                                                      (bases 1 to 1123)
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WFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQMARVGYYRQYCRQLGVDPGPNL
                                                                                                                                                                                                   PLN 29-JUL-2004
complete cds.
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                                                                                                                                                                                                                                                                                                                       Zea diploperennis
Zea diploperennis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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(chiB) gene,
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Zea diploperennis isolate d7 chitinase
AYS32741
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/cultivar="Ames21884"
                              GCTCGGCGTCGACGGCCCAACCTCACTTGCT
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join(<14. .446,569. .>972)
/gene="chiB"
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Genetics 167 (3), 1331-1340 (2004)
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<14. .>972
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Matches 724; Conserv
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                                   111
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DEFINITION
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                                                                                           //FOCESTIN 148-MANTATOROOZ 1."

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Pred. No. 1e-66;
0; Mismatches 18; Indels 129;
join(14. .452,579. .982)
/gene="chiB"
/codon_start=1
                                                                                   product="chitinase"
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/mol_type="genomic DNA" /usolate="M005" /isolate="M1" /dbc="taxon:4576" gene	Ouery Match 74.7%; Score 562.6; DB 8; Length 1122; Best Local Similarity 82.9%; Pred. No. 5.9e-66; Matches 724; Conservative 0; Mismatches 19; Indels 130; Gaps 2; Qy 6 GCAGAACTGCGGCCAAACGTATGCTGAGCAAACTTCGGCTACTCGGGAAAC 65	12 22 1'8 28	Qy 186 CAAGAACCAGGCGGAGCGGGAGCGGCAAGAACTTCTACACCCGGAGCGCGTTCCT 245 Db 283 CAAGAGCCAGGCGAGAGCAGGACATTCTACACCCGGAGCGCGTTCCT 342 Qy 246 GAGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGCAAGCG 305 Db 343 GAGCGCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTCAAGGCAAGCG 402	Qy 350 CGAGATCGCCGCCTTCTTCGCGCACGCACGAGACCGGCC
Db 283 CAAGAACCAGGCGGGGCAAGAACTTCTACACCCGGAGGGGTTCCT 342 Qy 246 GAGCGCGTCAAGGCGTTCCCCCATGGCGGTCACAGGTGCAAGCG 305 Db 343 GAGCGCTTCTCCAGGCTTCGCCCATGGCGGGCAGGCAAGCG 402 Qy 306 CGAGTCCCTCTTCGCGCACCACGCGCGCACGAGGCAGGCA	424 GCGGGGCAGAAGTACTACGGGCCGCCGCTGCAGATCTCGTGGAACTACAACTACGGGGGGCGCGCGC	544 763 604 823 764	Ancecegeceantaneographical properties of the control of the contro	RESULT 15 AY532736 AY532736 LOCUS DEFINITION Zea diploperennis isolate d1 chitinase (chiB) gene, complete cds. ACCESSION VERSION VERSION AY532736 A

Search completed: May 23, 2005, 14:20:15 Job time: 2457.33 secs

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Compugen Ltd.
GenCore version
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(without alignments)	12695.850 Million cell updates/sec	
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1 tcgatgcagaactgcggctg......ggcccaacctcacttgctga 753 US-10-692-367-69 753 Perfect score: Sequence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

8780412 Total number of hits satisfying chosen parameters: 4390206 segs, 2959870667 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004bs:* genesegn1990s:* genesegn2000s:* genesegn2001as:* N_Geneseq_16Dec04:* 1: geneseqn1980s:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004as: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ads92685 Chitinase	Ads92667 Chitinase	Ads92671 Chitinase		Ads92697 Chitinase	Ads92651 Chitinase	Ads92659 Chitinase	Aaa96222 cDNA erco	Ads92637 Chitinase	Ads92683 Chitinase	Ads92669 Chitinase	Ads92665 Chitinase	Ads92695 Chitinase	Ads92673 Chitinase	Ads92647 Chitinase	Ads92663 Chitinase	Ads92687 Chitinase	Ads92689 Chitinase		Ads92643 Chitinase
ID	ADS92685	ADS92667	ADS92671	ADS92693	ADS92697	ADS92651	ADS92659	AAA96222	ADS92637	ADS92683	ADS92669	ADS92665	ADS92695	ADS92673	ADS92647	ADS92663	ADS92687	ADS92689	ADS92677	ADS92643
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% Query Match Length DB	753	753	753	753	753	753	753	1094	753	765	753	753	750	753	753	771	774	771	771	753
% Query Match	100.0	97.2	96.4	96.0	95.5	95.3	95.1	95.0	94.9	94.5	94.5	94.5	94.1	93.2	93.2	92.7	92.5	92.0	91.6	91.5
Score	753	732.2	725.8	722.6	719.4	717.8	716.2	715.6	714.6	711.8	711.4	711.4	708.2	701.8	701.8	697.8	696.4	693	689.8	689
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ALIGNMENTS

Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium; True T, Simmons CR, Yalpani N; Chitinase variant polynucleotide #32. (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC. BP. 22-OCT-2002; 2002US-0420666P. 06-NOV-2002; 2002US-00290086. 14-MAR-2003; 2003US-00389432. 22-OCT-2003; 2003WO-US033588. ADS92685 standard; DNA; 753 (first entry) WPI; 2004-365417/34. P-PSDB; ADS92686. WO2004037194-A2. 02-DEC-2004 06-MAY-2004. Muller ML, Heterodera. Synthetic. ADS92685; RESULT 1 ADS92685

New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

Claim 4; SEQ ID NO 69; 197pp; English.

The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or nematched comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The

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                      Chitinase;
                                         Heterodera
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                                                                                                                                                                      Gaps
                                      This sequence represents
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCGCGAGATCGCCGCCTTCTTCGCGCACGCCACGAGACCGGGCCATT
                                                                                                                               Length 753;
fungus is from the genus Fusarium. The nematode is from the Heterodera. The polynucleotides and polypeptides are useful plant resistance to a fungus or nematode. This sequence repr
                                                                                             Sequence 753 BP; 141 A; 245 C; 261 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                  Indels
                                                                                                                             100.0%; Score 753; DB 13;
100.0%; Pred. No. 1.9e-132;
ive 0; Mismatches 0;
                                                         chitinase variant polynucleotide of the invention
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Best Local Similarity 100..
These 753; Conservative
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ds; plant resistance; fungus; nematode; Fusarium;
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Pred. No. 1.5e-128;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity 98.3
Matches 740; Conservative
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Length 753; 0 Other;

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360

420 420 480 480 540 540 909 9 9 999 720

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121 GGCAGCAGTGGCGGCGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAAC
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                            DB 13;
 G; 109 T; 0 U;
                        Score 725.8; DB 13;
Pred. No. 2.4e-127;
0; Mismatches 17;
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  C; 255
                          Query Match
Best Local Similarity 97.7%;
Matches 736; Conservative
 Sequence 753 BP; 144 A; 245
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GACGCCGTGGTGCGTTCAAGGCGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTG
                                                                                                                                                                        GGGCCCGCGGGGAGGACATCGGCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGCGG
                                                                                                      GACCCCGTGGTGCAAGCCGCCCTCTGGTTCTGGATGAACAACGTGCACCGTGTG
                                                                                                                                                         ATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGG
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                                                                                                                                                                                                                                                                 GGCGTCGACCCAGGGCCCAACCTCACTTGCTGA 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Chitinase variant polynucleotide #25.
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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in enhancing
                                                                                                                                                                                                                                                                             The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.3%; Score 717.8; DB 13; Length 753; Best Local Similarity 97.1%; Pred. No. 7.7e-126; Matches 731; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 753 BP; 140 A; 247 C; 260 G; 106 T; 0 U; 0 Other;
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                                                                                                                                 Simmons CR,
                                                                                       (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC.
                            22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
22-OCT-2003; 2003WO-US033588
                                                                                                                                                           WPI; 2004-365417/34.
P-PSDB; ADS92652.
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                                                AACAACCCCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTC 720
                                                                                                           The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypetides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                               ATGCCGCAGGCCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                                                                                                                                   Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 95.1%; Score 716.2; DB 13; Local Similarity 96.9%; Pred. No. 1.5e-125; Nes 730; Conservative 0; Mismatches 23;
                                                                                                                                                                   CGCGTCGACCCAGGCCCAACCTCACTTGCTGA 753
                                                                                                                                                    753
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                                                                                                                                                       GCCGTCGACCCAGGCCCCAACCTCACTTGCTGA
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                                                                                                                                                                                                                                                                                                                                                     Chitinase variant polynucleotide #19.
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                                              The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18899, and AAB18902-05), and glucosyl hydrolase famiy 18 chitinases (AAB18895, AAB18895, AAB18895, AAB18895, AAB18895, AAB188960-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence shuffling
                                                                                                                                                                     New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 715.6; DB 3; Length 1094; Pred. No. 2e-125;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1094 BP; 226 A; 339 C; 368 G; 161 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                      modulating its expression in plants.
                                                                                                                                                                                                                                   Claim 1; Page 64-65; 96pp; English.
                                                             (PION-) PIONEER HI-BRED INT INC
09-MAR-2000; 2000WO-US006121.
                              99US-0125915P
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                              24-MAR-1999;
                                                                                            Simmons CR,
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749 GCAGGGGTTCGGCGCCACCACCAGGGCCATCAACGGCGCCCTCGAGTGCGGCGCGGAACAA
                                                                  CCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; plant resistance; fungus; nematode; Fusarium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 753 BP; 132 A; 247 C; 269 G; 105 T; 0 U; 0 Other;
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                                                                                                                                                                                                                               CGACCCCGGGCCCAACCTCACCTGCT 894
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(PION-) PIONEER HI-BRED INT INC.
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PIONEER HI-BRED INT INC.
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                                                                                                                                                                               The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polymucleotide of the invention.
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                                                              New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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Matches 741; Conservative
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(PION-) PIONEER HI-BRED INT INC.
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14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The Hugus is from the genue Rusarium. The nematode is from the genue Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCGATGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGG 60
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                                                                                                                                                                                                         Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
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TGCCGCCAGCTCGACCCAGGGCCCAACCTCACTGCTGA 753
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ilarity 96.5%; Pred. No. 1.2e-124;
Conservative 0; Mismatches 26;
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                                                                                                                                                                            Chitinase variant polynucleotide #24.
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                                                                                                          encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Fusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                  gene; ds; plant resistance; fungus; nematode; Pusarium;
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                                                                                                                     Chitinase variant polynucleotide #37
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14-MAR-2003; 2003US-00389432
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The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Plearium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistence to a fungus or nematode. This sequence represents a chitinase variant polymucleotide of the invention.
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                                                                                                                                                                                                                                                                  93.2%; Score 701.8; DB 13; Length 753; 95.8%; Pred. No. 7.8e-123; Live 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                             Sequence 753 BP; 136 A; 250 C; 260 G; 107 T; 0 U; 0 Other;
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14-MAR-2003; 2003US-00389432.
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                                                                                                                                           gene; ds; plant resistance; fungus; nematode; Fusarium;
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                                                                                              Chitinase variant polynucleotide #13.
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14-MAR-2003; 2003US-00389432.
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Sequence 1, Application US/09522714

Sequence 1, Application US/09522714

Sequence 1, Application US/09522714

Sequence 1, Application US/09522714

Fater No. 6553020

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Masser

TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

FILE REFERENCE: 1100

CURRENT PILLING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/125,915

EARLIER FILLING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PastSEQ for Windows Version 3.0
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Pred. No. 7.3e-142;
); Mismatches 19;
US-09-522-714-5
US-09-522-714-23
US-09-522-714-23
US-09-522-714-17
US-09-522-714-17
US-09-522-714-17
US-08-812-025-9
US-09-138-813A-9
US-09-522-714-11
US-09-522-714-11
US-09-522-714-13
US-08-181-271A-38
US-08-181-271A-38
US-08-449-315-38
US-08-445-6255A-38
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CAAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCCT
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Sequence 29, Application US/09522714

Sequence 29, Application US/09522714

Parent No. 6563020

GRNERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

FILE REPERBNCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714

CURRENT PILING DATE: 1999-R: 60/125,915

SARLIER FILING DATE: 1999-R: 60/125,915

SARLIER FILING DATE: 1999-R: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 881
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US-09-522-714-29
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ORGANISM: Zea mays
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                                                          CGAGATCAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCCGC 425
   CGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCC
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Fatent No. 6563020

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Maize Chitinases and Their Use in

TITLE OP INVENTION: Enhancing Disease Resistance in Crop Plants

TITLE REPERENCE: 1100

CURRENT APPLICATION NUMBER: US/09/522,714

CURRENT APPLICATION NUMBER: 60/125,915

EARLIER PILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 1048
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; LOCATION: (42)...(854)
US-09-522-714-21
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ORGANISM: Zea mays
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Alexander, Danny C.
Beck, James J.
Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Payne, George B.
Sperison, Christoph
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                               CGCCTTCTTCGCGCATGTCACGCACGAGACCGGGCATTTGTGCTACATCAACGAGGTCG 180
                                                                                                                                     GCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCCGCGGGGCAGA 433
                                                                                                                                                                    TCGCCCCCACCATCAGGCCCATCAACGGCGCGCTCGAGTG---CGACGGGAACAACCCCG 670
             TCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGGCAAAGCGCGAGATCG 313
                                                                          COGCCTTCGCGCACGCACGCACGAGGCCGGCCATTCCTGTTACATCAGCGAGATCA 373
                                                                                                                                                                                                    AGTACTACGGGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGA 493
                                                                                                                                                                                                                                   241 GTTACTACGGGCGCGGCCGCTGCAGCTGTGCAACTACAACTACGGGCCGGCGGGGA 300
                                                                                                                                                                                                                                                                 GGGACATCGGCTTCGACGGGCTCGGGACCCCGGCAGGGTGGCGCGGGACGCCGTGGTGG 553
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                                                                                                                                                                                                                                                                                                                               CGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCCGCAGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAAC
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Sequence 31, Application US/09522714

Patent No. 6563020

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Maize Chitinases and Their Use in

TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

TITLE REFERENCE: 1100

CURRENT PELLING DATE: 2000-03-10

CURRENT FILING DATE: 2000-03-10

EARLIER APPLICATION NUMBER: 60/125,915

EARLIER FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PESTERO for Windows Version 3.0

SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
40.9%; Score 308.2; DB 4; Length 1
Best Local Similarity 66.7%; Pred. No. 4.9e-56;
Matches 550; Conservative 0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGGCCCAACCTCACTTGCT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGGCTCGACCTCAGTTGCT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PEATURE:
| NAME/KEY: intron
| LOCATION: (445)...(512)
| NAME/KEY: CDS
| LOCATION: (42)...(444)
| NAME/KEY: CDS
| LOCATION: (513)...(922)
| US-09-522-714-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1116
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534

700 594 760 648 708

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Query Match 26.6%;
Best Local Similarity 58.5%;
Matches 439; Conservative 0
             LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE CHARACTERISTICS:
                                                                                                                               US-08-181-271A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724
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APPLICANT: Stinson, deffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                          ZUDNATA:

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PARENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/08/181,271A

FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/093,301
FILING DATE: 16-7UL-1993
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/937,197
FILING DATE: 1-AFR-1991
PRIOR APPLICATION UNDER: US 07/678,378
FILING DATE: 1-AFR-1991
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/165,667
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/165,667
FILING DATE: 9-AFR-1989
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/165,67
FILING DATE: 1-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/632,441
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/68,122
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/68,122
FILING DATE: 5-MAR-192
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/68,122
FILING DATE: 27-8EP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/68,122
FILING DATE: 27-8EP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 27-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/369,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/369,677
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/369,677
FILING DATE: 12-APR-1993
ATTONNEY AFER: US 07/369,777
APPLICATION NUMBER: US 07/369,677
FILING DATE: 12-APR-1993
ATTONNEY AFER: US 07/369,777
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                STREET: 7 Skyline
CITY: Hawthorne
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 GGAGG------GTCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 Arcaaccaagcregraargerrececegegaaaagarreracacecereacrerriteerr 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 AATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
                                                                                                                                     99
                                                                                                                                                                             7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
                                                                                                                                                                                                                                                                   67 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTTCGGGCGGCGGCGGCAGC
                                                                                                                                                                                                                                                                                                                                   153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGAGGTAGTGGAACCCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                 127 AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGGCATC
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                                                                    30;
   Length 1079;
                                                                    Indels
Score 200.4; DB 1;
Pred. No. 2.5e-33;
0; Mismatches 281;
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; Sequence 37, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Beander, Danny C.
; APPLICANT: Beck, James J.
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213 GGAGG------GTCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 garecaracrecegererrecarecearcacerecerreracaceracaceceaece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609 ccaacrdradcrrrcagercegerrrerefriregargaaragceraaggceerrere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 AACCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 CAGAACTGCGGCTGCCAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 AGTGGCGCCGCTGCTGCGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 CCCGCGGGGGAGGGACATCGGCTTTCGACGGCTCGGGGACCCCCGGCAGGGTGGCGCGGGAC
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FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 619825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (919) 541-8619
TELEFRAX: (919) 541-8619
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE GRARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
RIUNG DATE: 1-APR-1991
APPLICATION NUMBER: US 07/576,566
FILING DATE: 6-FEB-1989
FILING DATE: 6-FEB-1989
FRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-FEB-1989
RROR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1991
APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1998
RROR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1998
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 1-APR-1993
FRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UNBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-OUT 1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-OUT 1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/329,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                    Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                   Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
   Duesing, John H.
Priedrich, Leslie B.
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                    Moyer, Mary B.
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DNA SEQUENCES AND USES THEREOF
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,803

FLING DATE: 19-MAY-1995

CLASSIPICATION NUMBER: US/08/444,803

PILING DATE: 13-MAY-1995

PILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/576,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION NUMBER: US 07/305,566

FILING DATE: 8-MAY-1988

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAY-1988

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAY-1988

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 1-APR-1998

PRIOR APPLICATION NUMBER: US 07/165,667

FILING DATE: 1-APR-1998

PRIOR APPLICATION NUMBER: US 08/042,847
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
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PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIBA-GEIGY Corporation
                                                                                                                                                                                                                                 Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    Sequence 37, Application US/08444803
Patent No. 5654414
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward, Eric R.
Williams, Shericca C.
                                                                                                                                                                                                                                                                                                                                           Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                               Alexander, Danny C.
Beck, James J.
Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                  Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                          Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CH
TITLE OF INVENTION: DN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hawthorne
STATE: New York
COUNTRY: USA
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                                                                          RESULT 7
US-08-444-803-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 carcarácricos retrocareceare de enecerto de enceracio de enceracio de enceracio de enceraciones en encerac
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                                                                                                                                                                                               PRIOR PELICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR PAPELICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
FILING DATE: 12-APR-1993
ATTORNEY AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 6-19825/PI/CGC 1727
TELECOMMUNICATION:
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58.5%; Pred. No. 2.5e-33;
iive 0; Mismatches 281;
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TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                       27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1079 base pairs
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Best Local Similarity 58.5
Matches 439; Conservative
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STRANDEDNESS: single
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 27-SEP-
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FILING DATE:
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US-08-449-043-37
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609 CCAACTGTAGCTTTCAGGTCGGGTTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                                                            669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGG----AATGGAATGTAACGGTGGT 725
                                                                                                                                        664 AACCCCGCCCAGATGAACGCGCGCATCGGCTACAAGCAGTACTGCCGCCAGCTCGGC 723
                                                                                                                                                                              726 AATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
                                                             604 CCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAAC 663
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APPLICANT: Nothaus, Jean-Marc
APPLICANT: Sparieson, Christoph
APPLICANT: Sparieson, Christoph
APPLICANT: Stateson, Jeffrey R.
APPLICANT: State R.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 SKyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTOTE: BM PC compatible
COMPTOTE: BM PC compatible
COMPTOTE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURNER: 24-MAY-1995
CLASSIPICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
RIGHT APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 13-JUL-1993
FILING DATE: 16-JUL-1993
FILING DATE: 6-NOV-1992
PHING DATE: 6-NOV-1992
PHING DATE: -NOV-1992
FILING DATE: 1-APR-1991
FILING APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
FILING RAPPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duesing, John H.
Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/08449043
Patent No. 5689044
GENERAL INFORMATION:
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Alexander, Danny C.
Beck, James J.
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CITY: Hawthorne
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
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PRIOR APPLICATION UNDERER:
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PRIOR APPLICATION NUMBER:
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58.5%; Pred. No. 2.5e-33;
trive 0; Mismatches 281;
                                                                                                                                  PRIOR DATE:
PRIOR DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
PILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
PILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
                                                         US 08/042,847
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                             6-APR-1993
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Best Local Similarity 58.5
Matches 439; Conservative
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STRANDEDNESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 6-APR-1
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127 AGTGGCGGCGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGGCATC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATIGCIACCAIGTITGCICATITCACTCACGAGACCGGACATITCIGCIACATAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAT --- CAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCC 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 gargearacriecegrerrecarecegarcaecerrerreracaegracrecaece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 36,21
REPERBUCE/DOCKET NUMBER: 5-19825/F1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.6%; Score 200.4; DB 1;
58.5%; Pred. No. 2.5e-33;
tive 0; Mismatches 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                               PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0071 1999
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-WAR-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
FILING DATE: 7-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/560,431
FILING DATE: 7-5EP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-WAR-1989
FILING DATE: 24-WAR-1989
FILING DATE: 24-WAR-1989
FILING DATE: 12-APR-1983
FILING DATE: 12-APR-1983
FILING DATE: 12-APR-1983
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                             UMBER: US 08/042,847
6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919)541-8587
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 6-APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 439; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-456-265A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                       669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGG---AATGGAATGTAACGGTGGT 725
  429 gagartaacogagcaacacgtaactactoccagagcagcaacacacaatacccatorofoca 488
                                                        GCGGGGCAGAAGTACTACGGGCGCGCCGCTGCAGATCTCGTGGAACTACAACTACGGG 483
                                                                                                            489 CCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTATCATGGAACTACAACTACGGA 548
                                                                                                                                                                                                             549 gégrgrgércaaagrerégérerréaéerréracéecagéécéaaerrérégerageaae 608
                                                                                                                                                                                                                                                                   544 GCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATG 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726 AATTCCGGTGCAGTCGCAAGGATTGGATACTATAGAGACTATTGTGGACAGACTGGT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ryals, John A.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     815
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CLASSIFICATION 1435
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-JAN-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-UOV-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
FRIUNG DATE: 1-APR-1991
FRIUNG DATE: 1-ERR-1991
FRIUNG DATE: 6-FEB-1999
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 6-FEB-1999
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1999
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08456265A Patent No. 5767369 GENERAL INFORMATION: APPLICANT: Alexander, Danny C.
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MOLECULE TYPE:
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609 CCAACTGTAGCTTTCAGGTCGGGTTTGTGGTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                          424 GCGGGGCAGAAGTACTACGGGCGCGGCCCGCTGCAGATCTCGTGGAACTACAACTACGGG 483
                                                                                              489 cceceananeccractrocorcorectecarccancraterrecancracantaceca 548
                                                                                                                                                                         549 GCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608
                                                                                                                                                                                                                  544 GCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATG 603
                                                                                                                                                                                                                                                                                            604 CCGCAGGCCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAAC 663
                                                                                                                                                                                                                                                                                                                       669 AACCAAGGSTTTGGAGCCACCATTAGAGCTATTAATGG---AATGGAATGTAACGGTGGT 725
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                                                                                                                                     484 CCCGCGGGGAGGACATCGGCTTCGACGGGTCGCGGGACCCCGGGCAGGTGGCGCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Shericca C.
IITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
IITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPARE: BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILLING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 GTCGACCCAGGGCCCAACCTCACTTGCTGA 753
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13.-JAN-94
APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 Skyline Drive
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
STREET: 7 SKyline Dr
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STATE: New York
COUNTRY: USA
ZIP: 10532
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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93 CAAAACTIGCGGTTGCGCTCCCAAACCTCTGTTGCAGTTCGGTTACTIGTGGTACCGAC 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GGAĞG-----GTCGĞTCGGTAĞCATTGTGACACAAGGTTTCTTTAACAATÄTT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-19825/P1/CGC 1727
PILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
PILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
PILOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,667
APPLICATION NUMBER: US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRICE APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRICE APPLICATION NATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRICE APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRICE APPLICATION NUMBER: US 07/580,431
APPLICATION NUMBER: US 07/580,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1079;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFCATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRILING DATE: 6-APR-1993
PRILING DATE: 6-APR-1993
PRILING DATE: 21-DEC-1990
PILING DATE: 21-DEC-1990
PRILING DATE: 21-DEC-1990
PRILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA: WORDER: US 07/425,504
PRILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA: US 07/848,506
PRIOR APPLICATION DATA: US 07/848,506
PRIOR APPLICATION DATA: US 07/68,122
PRIOR APPLICATION DATA: US 07/768,122
PRIOR APPLICATION DATA: US 07/768,122
PRIOR APPLICATION NUMBER: US 07/580,431
PRIOR APPLICATION DATA: US 07/580,431
PRIOR APPLICATION DATA: US 07/368,672
PRIOR APPLICATION DATA: US 07/368,672
PRIOR APPLICATION DATA: US 07/368,672
PRIOR APPLICATION DATA: US 07/369,018
PRIOR APPLICATION DATA: US 07/329,018
PRIOR APPLICATION DATA: US 07/329,018
PRIOR APPLICATION DATA: US 08/045,957
PRIOR APPLICATION DATA: US 08/045,957
PRIOR APPLICATION NUMBER: US 08/045,957
PRIOR APPLICATION NUMBER: US 08/045,957
PRICEROMONICATION NUMBER: S-19825/PI/CGC 1727
TELECOMONICATION INFORMATION:
NAME: BIMEY, James SCOCT
REFERENCE TO NUMBER: S-19825/PI/CGC 1727
TELECHOMONICATION INFORMATION:
MARE: BIMEY, James SCOCT
REFERENCE TO NUMBER: S-19825/PI/CGC 1727
TELECHOMONICATION INFORMATION:
MARE: ELECHOMONICATION INFORMATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 200.4; DB 1;
Pred. No. 2.5e-33;
0; Mismatches 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/937,197
PRIJING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATE: THE OFFICE 
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Best Local Similarity 58.5%;
Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (919)541-8689
INPORMATION FOR SEQ. ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-455-244-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 CCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCTATCATGGAACTACAACTACGGA 548
              484 CCCGCGGGGAAGGACATCGGCTTCGACGGGCTCGGGGACCCCCGGCAGGGTGGCGGGGAC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 GCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 ccaacreraccrircacercecerricicerriricanicalaaaracciaaaccecerrcic 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 CCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAAC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGG---AATGGAATGTAACGGTGGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 AACCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            726 AATTCCGGTGCAGCTCAACGCATGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
                                                                                                                                                          AGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGGCAAGCGC 306
                                                                                                                                                                                                                                              GAGATCGCCGCCTTCTTCGCGCACGCCACGCACGAGACCGGGCATTTCTGTTACATCAGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                               369 GAAATTGCTACCATGTTTGCTCATTTCACTCACGAGACCGGACATTTCTGCTACATAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAT --- CAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 GAGATTAACGGAGCAACACTAACTACTGCCAGAGCAGCAACACAATACCCATGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 GCGGGGCAGAAGTACTACGGGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 gégngnégrcaaagreréggrerngácerréhaggceágcégaacrngrégggrageaae 608
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                              321 AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         724 GTCGACCCAGGCCCAACCTCACTTGCTGA 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryals, John A.
Alexander, Danny C.
Beck, James J.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr.; Frederick
Montoya, Alice
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Patent No. 5789214
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skyline Drive
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
STREET: 7 SKyline Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-08-455-244-37
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                      261
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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DAS SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTOWNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 6-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICKATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 2-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
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FILING DATE: 7-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-7AN-94
APPLICATION NUMBER: US 08/093,301
PRIOR APPLICATION DATE: 16-7UL-1993
PRIOR APPLICATION DATE: 05/093,197
PRIOR APPLICATION NUMBER: US 07/937,197
PILING DATE: 6-NOV-1992
                                                                                                             ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919)541-8614
TELEPAK: (919)541-8689
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                       USA
                                                                                                                                                                                                                          10532
                                                                                                                                                                                                   COUNTRY:
CAAAACTGCGGTTGCGCTCCAAAACCTCTGTTGCAGTTCGGTTACTGTGGTACCGAC 152
                                                                                                                                                                                                                                                                                         261 Arcaaccaagcraargerigcecesesaaagarircracacceseacrrrrcerr 320
                                                                                                                                                                                                                                                                                                                                                                   AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTAC------CAGACGT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GABATTGCTACCAIGTTTGCTCATTTCACTCAGAGACCGGACATTTCTGCTACATAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 CCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTATCATGGAACTACAACTACGGA 548
                                                                     GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTTGCCGCTCGGGCGGCGGCGGCGCAGC 126
                                                                                                               153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGAGGTAGTGGAACCCCGACC 212
                                                                                                                                                           127 AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCACCGGCTCCTTCTTCAACGGCATC 186
                                                                                                                                                                                                213 GGAGG------GTCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                 187 AAGAACCAGGCCGGGAGCGGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCCTG 246
                                                                                                                                                                                                                                                                                                                                       247 AGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGCAAGCGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATCGCCCCTTCTTCGCGCACGCCACGCACGAGACCGGGCATTTCTGTTACATCAGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 GCGGGGCAGAAGTACTACGGGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 CCCGCGGGGGAGACATCGGCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGCGGGAC 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 GCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATG 603
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Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Patent No. 5804693
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moyer, Mary B.
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APPLICANT: Ryals,
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US-08-454-876-37
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Harms, Christian
APPLICANT: Meins, Christian
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Jean-Marc
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Sperison, George B.
APPLICANT: Sperison, Jeffrey R.
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DAM SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA.
APPLICATION NUMBER: 06/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: 08 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-AFR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-REP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/768,122
PILING DATE: 27-SEP-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNN-1989
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FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Friedrich, Leslie B.
                     Goodman, Robert M.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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: USA
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                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                  127 AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGGCATC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 GGAGG------GTCGGTCGGTAGCATTGTGACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 AAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCCTG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 CCCGCGGGGGAGGACATCGGCTTCGACGGCTCGGGGACCCCGGGCAGGGTGGCGCGGGAC 543
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                                                                                                                                                                                                                                                        7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC 66
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                            30;
                                                                                                                                                              DB 1; Length 1079;
                                                                                                                                                                 Score 200.4; DB 1; Length 1
Pred. No. 2.5e-33;
0; Mismatches 281; Indels
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Patent No. 3847258
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Beck, John H.
                                                                                                                                                                 Query Match
Best Local Similarity 58.5%;
Matches 439; Conservative
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
  786 GTGGACCCTGGTCCTAACCTTAGTTGCTAA 815
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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FILING DATE: 8-WAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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6-MAR-1992
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                                                                                                                                                                                                                                                Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice
                                                                                                       Sequence 37, Application US/08456262 Patent No. 5851766
                                                                                                                                                                                                                                                                                                                                                                  Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                   Ryals, John A.
Alexander, Danny C.
                                                                                                                                                                                                                  Beck, James J.
Duesing, John H.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS ADDRESSE: CIBA-GEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCCGGAGCGCGTTCCTG 246
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               APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-AFR-1993
ATTONNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFRENCE/DOCKET NUMBER: 56,129
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGACCCAGGCCCAACCTCACTTGCTGA 753
                                                                                                                                                                 TELEPHONE: (919)541-8614
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 58.5
Matches 439; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
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US-08-457-364-37
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609 CCAACTGTAGCTTTCAGGTCGGGTTTTGTGGTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
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APPLICATION NUMBER: 08/181,271
FILING DATE: 13-0AN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELIAN APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US 07/678,378
1-APR-1991
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7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08456240 Patent No. 5856154
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Alexander, Danny C.
Beck, James J.
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COMPUTER READABLE FORM:
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FILING DATE: 1-APR-
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.6%; Score 200.4; DB 2; Length 1
58.5%; Pred. No. 2.5e-33;
tive 0; Mismatches 281; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 S-19825/P1/CGC 1727
                                                                                      PALLON NUMBER: US 07/580,431
PELING DATE: 7-5EP-190
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-193
ATTORNEY/AGENT INFORMATION:
NAMME: BIMER: James Scott
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 58.5
Matches 439; Conservative
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US-08-456-262-37
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726 AATTCCGGTGCAGTCAACGCATGGATACTATAGAGACTATTGTGGACAGGCTTGGT 785
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                                                                                                                                                                                                                 669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGG----AATGGAATGTAACGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 AACCCCCCCAGATGAACGCGCGTCGCTACTACAAGCAGTACTGCCGCCAGCTCGGC
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APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGILATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
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213 GGAGG------GrogicGGTGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AAGAACCAGGCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCCGGAGCGCGTTCCTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAGATTCTACACCCGTGACTCTTTCGTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGAGTACTGCGGCGACGGGTGCCAGTCGGCCCCGTGCCGCTCGGGCGCGCGGCGCGCAGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCATACTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGAGGTAGTGGAACCCCGACC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGGCATC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGGCAAGCGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTAC------CAGACGT 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAACC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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Pred. No. 2.5e-33;
0; Mismatches 281; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION VINBER: 36,129
REFERENCE/DOCKET NUMBER: 8-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
FILING DATE: 20-OCT 1989
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/86,122
FILING DATE: 7-SEP-1991
FILING DATE: 7-SEP-1991
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
FILING DATE: 24-MAR-1989
FILING DATE: 24-MAR-1989
FILING DATE: 12-APR-1993
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY AGENT INFORMATION:
AND ATTORNEY AGENT INFORMATION:
AND ATTORNEY AGENT ATTORNEY ATTORNEY AGENT AGENT AGENT ATTORNEY AGENT AGEN
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ 1D NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 58.5
Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA
US-08-456-240-37
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                                                                                                                                                                                                                                                                                                                            604 CCGCAGGCCTTCGGCCCCACCATCAGGGCCATCAACGGCGCGCTCCAGGCGCACGGGAAC 663
                                                                                                                                                                                                                                                                                                                                                                        669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGG---AATGGAATGTAACGGTGGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                      664 AACCCCCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  726 AATTCCGGTGCAGCAAGCATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
429 GAGATTAACGGAGCAACACGTAACTACTGCCAGAGCAGCAACACACAAATACCCATGTGCA 488
                                                                      549 GCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC
                                                                                                                                                                                                                                544 GCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACGTGTGATG
                                           424 GCGGGGCAGAAGTACTACGGCGCGCGCCCCTGCAGATCTCGTGGAACTACAACTACGGG
                                                                                                                                     484 CCCGCGGGGAGGGACATCGGCTTCGACGGCTCGGGGACCCCCGGCAGGTGGCGCGGGAC
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Search completed: May 23, 2005, 15:37:18 Job time : 120.87 secs

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May 23, 2005, 14:20:22 ; Search time 386.609 Seconds (without alignments) 11943.947 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5695437 seqs, 3066160638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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753
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	* Query Match	% Query Match Length DB	DB	ΩI	Description
1	753	100.0	!	19	US-10-692-367-69	
7	732.2	97.2		19	US-10-692-367-51	Sequence 51, Appl
m	729.2	96.8		18	US-10-389-432B-51	
4	725.8	96.4		13	US-10-692-367-55	55,
S	722.8	96.0	750	18	US-10-389-432B-55	Sequence 55, Appl
9	722.6	96.0		19	US-10-692-367-77	Sequence 77, Appl
7	719.4	95.5		19	US-10-692-367-81	Sequence 81, Appl
8	717.8	95.3		19	US-10-692-367-35	Sequence 35, Appl
σ	717.2	95.2		17	US-10-425-114-19751	
10	716.2	95.1		19	US-10-692-367-43	Sequence 43, Appl
1	715.6	95.0		15	US-10-304-928-1	Sequence 1, Appli

Appl Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	L2, A	Appl	Appl	Appl	Appl	Appl
35,	43,	67,	21,	49,	23,	49,	23,	79,	31,	57,	31,	57,	47,	71,	47,	73,	61,	27,	61,	83,	27,	29,	65,	59,	65,	63,	6571	63,	45,	39,	75,	45,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
US-10-389-432B-35 US-10-692-367-21	US-10-389-432B-43	US-10-692-367-67	US-10-389-432B-21	US-10-692-367-49	US-10-692-367-53	US-10-389-432B-49	US-10-389-432B-53	US-10-692-367-79	US-10-692-367-31	US-10-692-367-57	US-10-389-432B-31	US-10-389-432B-57	US-10-692-367-47	US-10-692-367-71	US-10-389-432B-47	US-10-692-367-73	US-10-692-367-61	US-10-692-367-27	US-10-389-432B-61	US-10-692-367-83	US-10-389-432B-27	US-10-692-367-59	US-10-692-367-65	US-10-389-432B-59	US-10-389-432B-65	ᅼ	US-10-425-115-65712	ᅻ	7	-10-692-	-10-692-367	US-10-389-432B-45
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750	750	765	750	753	753	750	750	750	753	753	750	750	171	774	168	771	771	753	768	771	750	771	774	768	771	774	1277	771	774	780	780	171
94.9	94.7	94.5	94.5		94.5	94.1	94.1	94.1	93.2	93.2	92.8	92.8	92.7	92.5	92.3	92.2	91.6	91.5	91.2	91.2	91.1	91.0	8.06	90.6	90.4	89.7	89.5	89.3	89.3	89.1	89.1	88.9
714.8	713.2	711.8	711.6	711.4	711.4	708.4	708.4	708.2	701.8	701.8	698.8	698.8	697.8	696.4	694.8	694.6	689.8	689	686.8	9.989	989	685	683.6	682	9.089	675.6	674.2	672.6	672.4	671.2	671.2	669.4
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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AACAACCCCGCCCAGATGAACGCGCGCGTCGGCTACTACAGGCAGTACTGCCGCCAGCTC 720
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                                                                                                                                                                                                                                                                                                                                                 Length
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Pred. No. 2.4e-183
0; Mismatches 13
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          PRIOR APPLICATION NUMBER: 10/290,086
PRIOR FILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SENGTH: 753
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.3%;
Matches 740; Conservative (
                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-51
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                                                     Gaps
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                   Length 753;
                                                     0; Indels
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US-10-622-367-51
i Sequence 51, Application US/10692367
i Publication No. US200500505581
i GENERAL INFORMATION:
i APPLICANT: Muller, Mathias L.
i APPLICANT: Simmons, Carl R.
i APPLICANT: Simmons, Carl R.
i APPLICANT: Yalpani, Nasser
i TITLE OF INVENTION: Novel compositions with chitinase
i TITLE OF INVENTION: Activity
i FILE REFERENCE: 549162000320
cURRENT FILING DATE: 2003-10-22
i CURRENT FILING DATE: 2003-10-22
i PRIOR APPLICATION NUMBER: 10/389,432
                   100.0%; Score 753; DB 19; 100.0%; Pred. No. 7.9e-189;
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                                                     0; Mismatches
                 Query Match
Best Local Similarity 100.
Matches 753; Conservative
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                                                                                                                                                           661 AACAACCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCGCCAGCTC
    541 GACGCCGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTGCACGTGTG
                                                                          ATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCGGCGGG
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APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Movel compositions with chitinase
TITLE OF INVENTION: activity
ITILE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: 10/389,432
FRIOR APPLICATION NUMBER: 10/389,432
FRIOR APPLICATION NUMBER: 10/290,086
FRIOR FILING DATE: 2002-11-06
FRIOR FILING DATE: 2002-11-02
FRIOR APPLICATION NUMBER: 60/420,666
FRIOR APPLICATION NUMBER: 10/220
FRIOR APPLICATION NUMBER: 5002-110-22
NUMBER OF SEQ ID NOS: 84
SOGTWARR: FARENCE (FOR Windows Version 4.0)
FRIENGHING TANDER: LENGTH TS3
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Pred. No. 1.2e-181;
0; Mismatches 17;
                                                                                                                                                                                                                                               721 GGCGTCGACCCAGGCCCAACCTCACTTGC 750
                                                                                                                                                                                                                        721 GGCGTCGACCCAGGCCCCAACCTCACTTGC 750
                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/10692367
Publication No. US20050050595A1
GENERAL INFORMATION:
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Best Local Similarity 97.7%;
Matches 736; Conservative
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; LOCATION: (1)...(753)
US-10-692-367-55
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US-10-389-432B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 750;
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Pred. No. 1.5e-182;
0; Mismatches 13; Indels
                                                                                                                       Sequence 51, Application US/10389432B

Publication No. US20040250309A1

GENERAL INFORMATION

APPLICANT: Simmons, Carl

APPLICANT: Simmons, Carl

APPLICANT: True, Thom

APPLICANT: True, Thom

APPLICANT: True, Thom

TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE

TITLE OF INVENTION: ACTIVITY

FILE REPRENCE : 48942200300

CURRENT APPLICATION NUMBER: US/10/389,432B

CURRENT APPLICATION NUMBER: 60/337,029

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR PILING DATE: 2001-01-07

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 750
Query Match
Best Local Similarity 98.3%;
Matches 737; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Unknown
                                                                                                              -10-389-432B-51
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241 TTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGGGGGC
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                                                181 GGCATCAAGAACCAGGCCGGGAGCGGGTGCGAGGGGCAAGAACTTCTACACCCCGGAGCGCG
                                                                                                               TTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCCATGGCGGGTCACAGGTGCAGGGC
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APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Activity
FILE OF INVENTION: Activity
FILE OF INVENTION: Activity
FILE REPERBER: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
THENGTH: 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTCGACCCAGGGCCCAACCTCACTTGC 750
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                                                                  ATCAGCGAGATCAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGC
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GENERAL INFORMATION:

APPLICANT: Muller, Mathias

APPLICANT: Simmons, Carl

APPLICANT: True, Thom

APPLICANT: True, Thom

TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE

CURRENT APPLICATION NUMBER: US/10/389,432B

CURRENT APPLICATION NUMBER: 06/337,029

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 66

SEQ ID NO S:

LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTCGACCCAGGGCCCAACCTCACTTGCTGA 753
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10.10-399-432B-55

1 Sequence 55, Application US/10389432B

2 Publication No. US20040250309A1
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                                                                                                                                                   1 TCGATGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGCTACGGCTACTGCGGC 60
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             OTHER INFORMATION: Variant sequence produced by shuffling techniques
                                                                                                               ö
                                                                                     Length 753;
                                                                                    Query Match 96.0%; Score 722.6; DB 19; Length Best Local Similarity 97.5%; Pred. No. 8.2e-181; Matches 734; Conservative 0; Mismatches 19; Indels
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                       ; FEATURE:
; NAME/KGY: CDS
; LOCATION: (1)...(753)
US-10-692-367-77
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Sequence 81, Application US/10692367; Publication No. US20050050595A1; GENERAL INFORMATION:
APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser

US-10-692-367-81

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                compositions with chitinase
TITLE OF INVENTION: Novel compositions with or TITLE OF INVENTION: activity
FILE REFERENCE: 54916200320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
FRIOR PILING DATE: 2003-10-40
FRIOR FILING DATE: 2003-11-06
FRIOR FILING DATE: 2002-11-06
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US-10-692-367-81
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; OTHER INFORMATION: Clone ID: LIB3151-014-E10_FLI
US-10-425-114-19751
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ORGANISM: Zea mays
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                                                                                                                                            Sequence 35, Application US/10692367

Publication No. US200500505A1

GENERAL INFORMATION:
APPLICANT: Mulhias L.
APPLICANT: Almone, Carl R.
APPLICANT: Simmone, Carl R.
FILE OF INVENTION: Acciduty 4
FILE OF INVENTION NUMBER: 10/389, 432
PRIOR PLING DATE: 2003-03-14
PRIOR PLING DATE: 2003-11-06
PRIOR PLING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PLING DATE: 2002-11-07
PRIOR PLING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 717.8; DB 19
Pred. No. 1.5e-179;
0; Mismatches 22;
                                                                   GGCGTCGACCCAGGGCCCAACCTCACTTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 97.1%;
Matches 731; Conservative
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NAME/KEY: CDS

LOCATION: (1)...(753)

US-10-692-367-35
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Sequence 19751, Application US/10425114
Sequence 19751, Application US/10405114
Sequence 19751, Application No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jinadong
APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Soreen, Steven E
APPLICANT: Go, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
SEQ UD NO 19751
LEMOREN OF SEQ ID NOS: 73128
SEQ 1D NO 19751
LEMORTH: 1037
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Score 716.2; DB 19;
Pred. No. 4e-179;
0; Mismatches 23; 1
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95.1%;
ilarity 96.9%;
Conservative
 Query Match
Best Local Similarity
Matches 730; Conserv
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                                                            CGAGATCGCCGCCTTCTTCGCGCACGCCACGAGACCGGGCATTTCTGTTACATCAG 365
                                                                                                                                                            GGGGCAGAAGTACTACGGGCGGGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCC 485
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                                                                                                                           CGCGGGGAGGGACATCGGCTTCGACGGGCTCGGGGACCCCCGGCAGGGTGGCGGGGACGC
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US-10-692-36/-43

Sequence 43, Application US/10692367

Publication No. US20050050581

GENERAL INFORMATION:
APPLICANT: Mathas L.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons Carl R.
APPLICANT: Simmons Carl R.
APPLICANT: NOWER: US/10/692,367

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/389,432

PRIOR FILING DATE: 2003-03-14

PRIOR PLING DATE: 2003-11-06

PRIOR PLING DATE: 2002-11-07

PRIOR PLING DATE: 2002-11-07

PRIOR PLING DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 84

SOFTWARE FREEKE FREEKE FOR WINGOWS Version 4.0

SEQ ID NO 43

LENGTH: 753
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; LOCATION: (1)
US-10-692-367-43
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                                                                                                                              1 TCGATGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGGC
                                                                                                                                                                                                                                                                                                      GGCAGCAGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAAC
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                                                 Gaps
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; Publication No. US20030101484A1
; GENERAL INFORMATION:
    APPLICANT: Simmons, Carl R.
    APPLICANT: Simmons, Carl R.
    APPLICANT: Submin, Nasser
    TITLE OF INVENTION: Maize Chitinases and Their Use in TITLE OF INVENTION: Bahancing Disease Resistance in Crop Plants; ITLE REPERENCE: 1100D
    FILE REPERENCE: 1000
    CURRENT APPLICATION NUMBER: US/10/304,928
    CURRENT FILING DATE: 2002-211-26
    PRIOR APPLICATION NUMBER: 09/522,714
    PRIOR PILING DATE: 5000-03-10
    PRIOR PILING DATE: 1999-03-24
                                                                                                 1 TCGATGCAGAACTGCGGCTGCCAGACGTATGCTGCAGCAGCAGGTTCGGCTACTGC
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Length 753
                                               23; Indels
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APPLICANT: Muller, Mathias
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                                                                                            ; NAME/KEY: CDS
; LOCATION: (51)...(893)
US-10-304-928-1
                                                                                                                                                              Similarity
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1
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ORGANISM: Zea mays
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RESULT 12
US-10-389-432B-35
Sequence 35, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:

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APPLICANT: Simmons, Carl
APPLICANT: True, Thom
APPLICANT: True, Thom
TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHI
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
FILE REPRENCE: 489492000300
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 35
LENGTH: 750
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                                                                                                                      Sequence 21, Application US/10692367
Publication No US20050050581
GENERAL INFORMATION:
APPLICANT: Minler, Mathias L.
APPLICANT: Simmons, Carl R.
CURRENT APPLICATION NUMBER: 10/290,086
PRIOR APPLICATION NUMBER: 10/290,086
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR APPLICATION NUMBER: SO02-10-22
NUMBER OF SEQ ID NOS: 84
SEQ ID NOS: 84
SEQ ID NO 21
SEG ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%; Score 714.6; DB 19
96.8%; Pred. No. 1.1e-178;
live 0; Mismatches 24;
                               721 CGCGTCGACCCAGGCCCCAACCTCACTTGC 750
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Best Local Similarity 96.8
Matches 729; Conservative
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CTHER INFORMATION: Variant sequence produced by shuffling techniques;
CTHER INFORMATION: 4N1/95_H3 nucleic acid
US-10-389-4328-43
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APPLICANT: Simmons, Carl
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 489492000300;
CURRENT APPLICATION NUMBER: US/10/389,432B
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE PARESEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 750
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; Publication No. US20040250309Al
; GENERAL INFORMATION:
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APPLICANT: MULIER, MACHIAS L.
APPLICANT: SIMMONS, CAT R.
TITLE OF INVENTION: Novel compositions with chitinase
TITLE OF INVENTION: Activity
FILE REPERBER: 549162000320
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 10/290,086
PRIOR FILING DATE: 2003-14
PRIOR FILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PLING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PLING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 67
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-07
PRIOR PLING DATE: 2001-07
PRIOR PLING DATE: 2001-07
PRIOR PLING DATE:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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, NAME/KEY: CDS

, LOCATION: (1).

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Mismatches
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Job time : 388.609 secs
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May 23, 2005, 12:20:11 ; Search time 2155.94 Seconds (without alignments) 13294.634 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMA ID BG8376563 AAY103546 CD6324436 CD6324434 CD9944342 CD994434 CD994434 CD994434 CD9944865 CD9944865 CD9944865 CD9994865 CD9994865 CD9994865 CD9991565 CCR00010	SUMMARIES	Description	BG837663 Zm10 01e1	AY103546 Zea mays	CO524416	CD435649 CD435649 EL01N0364	BG837479 BG837479 Zml0 10h	CD443492 EL01N042	CN133023 OX1 9 D1		BM895383 952073H05	CD995497 QBB25£07	CD994156 QBB13f07	CD994132 QBB13e04	CD994454	CD994869 QBB18d07		CD995176 QBB20h11	CA197556 SCBFAD106	: CF001565 QBG4f06.x	CD999920 QBG10a02.	CF000010 QBG11a02	CF000228 QBG13e12	CF000357 QBG15b09	CF000565 CBG17b11	
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		Score	663.4	643	619.6	599.6	598.6	550.8	546.8	536.8	533.2	526.6	522.6	521.2	520.6	519.6	519.6	508.6	502.4	498.8	498.8	498.8	498.8	498.8	498.8	000
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/note="Vector: Bluescript SK+/KhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-incoulated in the morning (~10 am) with 1 ml of a macroconidial sugpension (500,000 sporess/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was

CF000161 QBG12g06. CF000412 QBG15g11. CF000325 QBG14g11. CF002068 QBG84f07.x CF001260 QBG8h11.x CF001260 QBG2a02.x CF001260 QBG2a02.x CF001360 QBG2602.x CF001316 QBG2605.p CF001075 QBG2605.p CF001075 QBG2605.p CF0011507 QBG11a12.x CF0011507 QBG11a12.x CF0011507 QBG11a12.x CF0011507 QBG2a02.p CF001425 QBL14a03.x CF001425 QBL14a03.x CF001425 QBL14a03.x CF001425 QBC14a03.x CF001391 QBC36b07.x	indents i bp mRNA linear EST 25-MAY-2001 Pusarium_graminearum_corn_silk Zea mRNA sequence. reptophyta; Embryophyta; Tracheophyta; reptophyta; Poales; Poaceae; PACCAD	Clader's fallocoldead's Autoposonead's cas. Clades 1 to 855) Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moores,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A, Byprott,D. and Tinker,N.A. Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum Contact: Harris, Linda J. Contact: Harris, Linda J. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6, CANADA Tel: (613) 759-656 Email: harrisij@agr.gc.ca. Location/Qualifiers L. 455 /continyar="CO388" /db xref="taxon:4577" /clone="Zml0_olea!" /dev_stage="4" Adys post-silk emergence" /clone="Zml0_olea!" /clone="Zml0_AAFC_ECORC_Fusarium_graminearum_corn_silk" /clone=lib="Zml0_AAFC_ECORC_Fusarium_graminearum_corn_silk"
CF000161 CF000412 CF000412 CF000325 CF0002109 CF001262 CF001262 CF001300 CF001300 CF00175 CF0010775 CF011507 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634 CF0114634	ALIGNMENTS 855 bp AAFC_ECORC_Fusar 110_01e10, mRNA s 103986 slantae; Streptop	Tanger, Failt-Concase; Anuropogomeae; Ladacis failt-Concase; Anuropogomeae; Ladacis failt-Concase; L.J., Balcerzak, M., Allard, S., Sapa Moors, A., Hattori, J.I., Ouellet, T., Robert Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Maize Silk Si Channel Inoculation with Fusarium graminea Unpublished (2001) Contact: Harris, Linda J. Contact: Harris, Linda J. Contact: Harris, Linda J. Contact: Harris, Linda J. Contact: Marris, Marris, Marris, Ottaw J. Contact: Marris, Ma
5 2 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ALIC BSE LA Zml0_AAFC_ECOR Clone Zml0_01el0, GI:14203986 Viridiplantae; St	railcolueae; Anucologa 1.J., Balcerzak,M., A. L.J., Balcerzak,M., A. L.J., Balcerzak,M., A. L. and Tinker,N.A. Incollation with Fus. Babed (201) :: Harris, Linda J. Cercal and Oilseed R. tuce and Agri-food Cal control Agri-food Cal tuce and Agri-food Cal control Agri-food Cal tuce and Agri-food Cal control Agri-food Cal tuce and
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25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 BG837663/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE
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Direct Submission

Direct Submission

Direct Submission

Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interseted in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizeng.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or MCBI, www.ncbi.nlm.nlh.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, lows Etter, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGGCAG 125
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design Covergo Probes (2002).
                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizaDB:638921"
/db_xref="taxon:4577"
/clone lb="Maize Mapping Project/DuPont Cornsensus
Library"
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Pred. No. 7.8e-127;
0; Mismatches 45;
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 91.4%;
Matches 701; Conservative (
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                                                              Score 663.4; DB 4;
Pred. No. 3.5e-131;
0; Mismatches 21;
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/clone_lib="3530 - Full length cDNA library created by
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/note="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCNV-SPORT
6.1; Site_l: ECORV; Site_2: Not!; Maize Gene Discovery
project contracted with Invitrogen to produce a
normalized, full length library in a pSport vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables, poly(A) +
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
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CAACAGGGTGGCGCAGGACGCCGTGATCGCGTTCAAGACGGCGCTCTGGTTCTGGATGAA 747
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fisBute_type="multiple"
/dev_stage="varies_by_tissue"
/lab_nost="DH10B"
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Department of Biological Sciences
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/mol_type="mRNA"
/cultivar="B73"
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vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unique clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (http://www.genome.arizona.edu/orders/). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."
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GCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCACAAC GCAGAACTIGCGGCTGCCGAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC Gaps ö Length 767; Score 619.6; DB 7; Length Pred. No. 7.6e-122; 0; Mismatches 14; Indels 82.3%; Conservative Similarity Matches 628; Query Match Best Local S φ

RESULT 3 CO524416

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ò 셤 65

EL01N0364B04.b Endosperm_3 Zea mays cDNA, mRNA sequence. CD435649 GCAGGGGTTCGGCGCCACCACCAGGGCCATCAACGGCGCCCT 767 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 4 CD435649 LOCUS

EST 03-JUN-2003

linear

MRNA

GI:31351292 CD435649.1

Zea mays Zea mays

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Score 598.6; DB 4;
Pred. No. 2.3e-117;
6; Mismatches 56;
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Pax: (613) 759-6566
Email: harrislj@agr.gc.ca.
                                                                                                                                                                                                                                  BG837479.1 GI:14203802
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                         E 1 (Dases 1 to 737)
S Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.
Larkins, B., Becraft, P. and Messing, J.
Characterization of the maize endosperm transcriptome and its comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/close_lib="Endosperm 3"
/close_libe="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2: XhoI"
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Pred. No. 1.4e-117;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                               organism="Zea mays"
                                                                                                                                                                                                                                               Seq primer: T3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="W22"
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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morrhing (-10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."
                                                                                                                                                                                                                                                                                                                                              BG837479 Sml0_AAPC_ECORC_Fusarium_graminearum_corn_silk Zeamays_cDNA_clone Zml0_10h09_A Zml0_10h09, mRNA_sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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605 CGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harris, Linda J.
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 15; Gaps
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Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A, Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Incoulation with Pusarium graminearum
Unpublished (2001)
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1. 958
| roganism="Zea mays" |
| mol type="mrNa" |
| db xref="texon:4577" |
| clone="Zm10 loh09" |
| tissue type="4-5 days post-silk emergence" |
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Matches 571; Conservative
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1 (Dases 1 to 710)

S. Lai, D. Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.P., Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome

L. Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinsheng

Dr. Joachim Messing's lab

Waksman Institute, Rutgers University

190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
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                                  ACCGTGTGATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGT
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                     CD443492 11.b Endosperm_4 Zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
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/mol_type="mRNA"
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Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases: 1 to 817)
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTS: OX1 9 D11.b1 A002
Contact: Cordonnier-Pratt PM
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OX1_9_D11.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1_9_D11_A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 cereadececercaageceraeceagerrececarecearecegerecageraeceaa 424
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/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_4"
/note="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2: Xhoite="Vector: pBluesGript SK-; Site_1: BcoRI; Site_2: And Stream SK-; Site_1: BcoRI; Site_2: And SK-; Site_2: BcoRI; Site_2: And SK-; Site_2: BcoRI; Site_2: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGAACTGCGGCTGCCAGCCAAACGTCTGCTGCAGCAAGTTCGGGTACTGCGGCACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 550.8; DB 6;
Pred. No. 3.5e-107;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN133023
CN133023.1 GI:45963543
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665

725

605

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Jibrary was prepared by George Rudenko using poly (A) library was prepared by George Rudenko using poly (A) elected RNA and Universal Ribochone CDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo (dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-disested pull9 vector. Blue/white selection on carbenicillin-containing plates was used to recover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
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                                                                                                                                                             CGTGGTCGCGTTCAAGACGGCGCTCTGGTTCTGGACCAACAACGTGCACGGGGTGATGTC 717
                                                                                                                                                                                                                                                                             GCAGGGGTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGGCAACGCCAAGAA 777
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM736454 628 bp mRNA linear EST 01-MAR-2º
952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
                                                                      GCAGGCCTTCGGCGCCACCATCAGGGCCATCAACGCCGCGCGCTCGAGTGCGACGGGAACAA
                        CGCGGGGGAGGGACATCGGCTTCGACGGGCTCGGGGACCCCCGGCAGGGTGGCGCGCGGACGC
                                                                                                                                                                                                                                                                                                                                      666 CCCCGCCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clome_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
                                                                                                                          CGTGGTGGCGTTTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tisue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
phases"
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/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
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Fax: 650 725 8221
Email: walbot@stanford.edu
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Pred. No. 3.4e-104;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
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Stanford University
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mays cDNA, mRNA sequence.
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93.0%;
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Best Local Similarity 93.03
Matches 573; Conservative
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Unpublished (1999)
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Collivar="BTX623"
/Wol_type="MRNA"
/Collivar="BTX623"
/db Arsf="taxon:4558"
/dlone="OXI 9_D11 A002"
/lab host="BH10B-T1 phage-resistant E. coli"
/clone_lib="Oxidatively-stressed leaves and roots"
/clone_lib="Oxidatively-stressed leaves and roots"
/clone_lib="Oxidatively-stressed leaves and roots"
/clone_lib="Oxidatively-stressed leaves and roots"
/clone_lib="Oxidatively-stressed leaves and roots and from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different brail sites of the phases. The vector (5-prime DrailI site is CACCATGTG). Thou excises the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                           the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 GCAGAACTACGGCTGCCAGGCAGGTTACTGCTGCAGCAAGTTCGGTTACTGCGGCACGAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 CAAGAACCAGGCCGGGAGCGGGTGCGAGGCCAAGAACTTCTACACCCCGGAGCGCGTTCCT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAACCAGGCCGGGAACGGGTGCGAGGCAAGAACTTCTACACCCCGGAGCGCGTTCCT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGCAAGCG 305
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                                                                         Tel: 706 542 1860
Fax: 706 583 0010
Email: mmpratt@uga.edu
Libzary constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGCAAAC
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 2.5e-106;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                    Seq primer: Sugs (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.6%;
87.2%;
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Jibrary was prepared by George Rudenko using poly (A) elected RNA and Universal Ribochone CDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo(dI) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-octabiling plates was used to recover positive clones."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 16-JUL-2003
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/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stat
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/clone_lib="952 -
                                                                                                                                                                                                                                                                                                                                                     70.8%;
llarity 92.1%;
Conservative
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952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
BM895383.1 GI:19350851
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                                                                                                                                                                                                           GCCTTCTTCGCGCACGTCACGCACGACACTCTGCTACTACACACGCGAGATCAACA 241
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                                                                                             62 GCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCCTGAGCGCCCGTC 121
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               GCCGGGAGCGGGTGCGAGGGCAAGAACTTCTACACCCGGGAGCGCGTTCCTGAGCGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Location/Qualifiers
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238 123 298 183 358 243 418 303 478 363 538 423 598 483 658 543

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CD994156 578 bp mRNA linear EST 16-JUL-2003 QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA sequence. CD994156
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 578)
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Contact: Genoplante
Genoplante
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Location/Qualifiers
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Zea mays"
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| cultivat="F2" |
| db_xref="taxon:4577"
| clone="QBB13f07"
| tissue type="embryo"
| clone_lib="QBB"
                                                                                                                                                          GI:32854475
GCCCAACCTCACCTGCT 601
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                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACTACGGGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGAG 494
                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopeida, Poalee, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                   Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                   plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                              93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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Pred. No. 5e-102;
0; Mismatches 19; Indels 0
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/db_xref="texon:4577"
/clone="QBB25£07"
/t.ssue_type="embryo"
/clone_lib="QBB"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Zea mays"
                                      GI:32855816
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ilarity 96.6%;
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Genoplante
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CD994454 578 bp mRNA linear EST 16-JUL-2003
QBB15f08.xg QBB Zea mays cDNA clone QBB15f08, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoplante, a major partnership french program in plant genomics (pubblished (2003)
Contact: Genoplante Genoplante Genoplante
                                                                                                                  682 GCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGGCTCGGCGTCGACCCAGGGCCCAAC
                       GCGCCCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCGCCC
                                                                                             622 ACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAACAACCCCGGCCCAGATGAAC
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mol_type="mRNA"
Cultivat="Earach
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Best Local Similarity 96.44
Matches 532; Conservative
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    (Dases 1 to 575)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGGCAAGCGCGAGATCGCCGCCTTC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fins sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
                                                          481 AAGGGGGGGTGGGCTACTACAGGCAGTACTGCCGCCAGCTCGGCGTCGACCCCGGGCCC
Gaps
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QBB13e04.xg QBB Zea mays cDNA clone QBB13e04, mRNA sequence.
CD994132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
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cultivar="R2"
/db_xref="taxon:4577"
/clone="QBB13e04"
/tissue_type="embryo"
/clone_lib="QBB"
                                                                                                                                                                                                                                                                                                CD994132.1 GI:32854451
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Genoplante
                                                                                                                                 AACCTCACCTGCT 553
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CD994885 753 bp mRNA linear BST 16-JUL-2003
QBB18e05.xg QBB Zea mays cDNA clone QBB18e05, mRNA sequence.
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Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93...re Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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                                                                               301 GGCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGCGGGACGCCGTGGTGGCGTTCAAG
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                                                         AACGCCTACTGCGACCCGACCAAGAGGCAGTGGCCGTGCGCCGCGGGGCAGAAGTACTAC
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                                                                                                                                                                                                                                                                                                                                                                 622 ACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAACAACCCCGCCCAGATGAAC
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llarity 96.5%; Pred. No. 1.6e-100;
Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
/clone="QBB18e05"
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/clone_lib="QBB"
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/mol_type="mRNA"
/cultivar="F2"
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QBB18d07.xg QBB Zea mays cDNA clone QBB18d07, mRNA sequence.
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                                     ACGGGGGGCGCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGGCCCA 305
                                                                                                                                                            619
                                                                                                                                                                                 366 AGGCGCGCTCTGGTTCTGGATGAACAGCGTGCCNGGGGTGGTGCCGCAGGGGTTCGGCG 425
                                                                                                                                                                                                                                                        CCACCACGGGCCATCAACGGCGCCCTCGAGTGCGGGGGGAACAACCCCGCCCAGATGA 485
                                                                                                                                                                                                                                                                                                                680 ACCCCCCCATCCGCTACTACAAGCAGTACTGCCCCCAGCTCGGCGTCGACCCCAGGGCCCCA 739
                                                                                                                                                                                                                                                                                                                                   ACGCGCGCGTCGCCTACTACAGCAGTACTGCCGCCAGCTCGGCGTCGACCCCGGGCCCA 545
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                                                                                                                      TCGGCTTCGACGGGCTCGGGACCCCGGCAGGGTGGCGCGGGACGCCGTGGTGGCGTTCA 365
                                                                                                                                                                                                                                     CCACCATCAGGGCCATCAACGGCGCGCTCCGAGGGCGCGGGAACACCCCGGCCCAGATGA 679
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fix: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
Location/Qualifiers
1. 741
/organism="Zea mays"
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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                                                                                  TCGGCTTCGACGGGCTCGGGGACCCCGGCAGGCTGGCGCGGGACGCCGTGGTGGTCATCA
                                                                                                                                                            AGGCGCCCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCG
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/db xref="taxon:4577"
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/tissue type="embryo"
/clone_lib="QBB"
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                                                                                                 301 GGCTTCGACGGGCTCGGGGAACCCCCGGCAGGGTGGCGGGACGCCGTGGAGGGGACGCGGAGGGTTCAAG 360

        562
        GCGGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTGATGCCGCAGGGCTTCGGCGC
        621

        361
        GCGGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGGTGGTGCCGCAGGGGTTCGGCGC
        420

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                                                                                                                                                                                                                                              ACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGGAACAACCCCGGCCCAGATGAAC 681
                  TACCCAGGCTTCGCCCATGGCGGGTCACAGGTGCAGGGCAAGCGCGAGATCGCCGCCTTC 321
AGCGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCG 60
                                                                                                                                                             GCCTTCGACGGGCTCGGGGACCCCGGGAGGCGCGGGACGCCGTGGTGGTCGAG
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                                                                                                                                                                                                                                                                                                         CTCACTTGCT 751
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Search completed: May 23, 2005, 15:33:09 Job time : 2157.94 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

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May 24, 2005, 12:19:56; Search time 113.905 Seconds (without alignments) 848.864 Million cell updates/sec

US-10-692-367-70 Title:

Perfect score:

1 SMQNCGCQPNVCCSKFGYCG.....GYYKQYCRQLGVDPGPNLTC 250 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04: geneseqp1980s:* •• Database

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* geneseqp2000s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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•	Description	Ad892686	Ad892668	Ad892698	Ads92684	Ad892694	Ads92672	Ad892660	Ads92688	Ads92618	Ads92666	Aab18894	Ad892670	Ad892690	Ads92638	Ad892664	Ad892676	Ads92678	Ad892652	Ads92696	Ads92682	Ads92700	Ads92646	Ads92650	Ad892656	Ads92692
	ΩI	ADS92686	ADS92668	ADS92698	ADS92684	ADS92694	ADS92672	ADS92660	ADS92688	ADS92618	ADS92666	AAB18894	ADS92670	ADS92690	ADS92638	ADS92664	ADS92676	ADS92678	ADS92652	ADS92696	ADS92682	ADS92700	ADS92646	ADS92650	ADS92656	ADS92692
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	Score	1408	1377	1372	1366	1363	1360	1358	1357.5	1351	1351	1351	1350	1349	1348	1348	1344	1342	1341	1336.5	1335.5	1335	1328.5	1328.5	1325.5	1324.5
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ADS92674 ADS92662 ADS92680	ADS92648 ADS92628 ADS92634 ADS92644	ADS92654 ADS92636 ADS92640	ADS92658 ADS92624 ADS92617 ADS92635	ADS92633 ADS92642 ADS92632	ADS92620 ADS92630 ADS92622
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94.0 93.9	93.7 93.6 93.2	93.0 92.5	91.3 90.3 89.9	999	88 88 . 4 8 . 2
1323 1322.5 1321.5	1319 1318.5 1314.5 1312	1309.5 1303 1300.5	1283.5 1271.5 1265.5	1258.5 1255 1253	1245 1244.5 1242.5
26 27 28	3308	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3 3 3 4 6 3 9 8 7 6	444 0 H G	4 4 4 6 4 0

ALIGNMENTS

Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera. ADS92686 standard; protein; 250 AA. Chitinase variant polypeptide #32. 22-OCT-2002; 2002US-0420666P. 06-NOV-2002; 2002US-00290086. 14-MAR-2003; 2003US-00389432. 22-OCT-2003; 2003WO-US033588 (first entry) WO2004037194-A2. 02-DEC-2004 06-MAY-2004 Synthetic. ADS92686;

:

Simmons CR, Yalpani N; True T, Muller ML,

VERDIA INC. PIONEER HI-BRED INT INC.

(VERD-) (PION-) WPI; 2004-365417/34. N-PSDB; ADS92685 New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

Claim 3; SEQ ID NO 70; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.

Sequence 250 AA;

Sequence 250 AA;

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                                                                                                                                                                                                                                          DAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240
                                                                                                                                                                                                                                                              ISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
                                                                                                                                                                                                   ISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
                                                                                                                      GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or enematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                            9
                                                                              SMONCGCQPIVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN 60
                                                                                                                                       GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKRRIAAFFAHATHETGHFCY
                                                            SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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 Length 250;
                               Indels
100.0%; Score 1408; DB 8; 100.0%; Pred. No. 1.6e-115;
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                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         ADS92668 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitinase variant polypeptide #23.
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
               Best Local Similarity 100.
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                      GVDPGPNLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-365417/34.
N-PSDB; ADS92667.
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                                                                                                                                                                                                                                                      The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                             9
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                                                                              SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
                                                                                                                                                                               ISBISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR
                                                             1 SMQNCGCQPNVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
                                                                                                                      GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY
                                                                                                                                                                                                                                        DAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL
                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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Length 250;
                                Indels
Score 1377; DB 8;
Pred. No. 8.6e-113;
4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 82; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      ADS92698 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinase variant polypeptide #38.
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 97.8%;
97.2%;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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               Best Local Similarity 97.2
Matches 243; Conservative
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N-PSDB; ADS92697.
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chitinase variant polypeptide of the invention.
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                                                                                                              GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY 120
                                                                                                                           GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY 120
                                                                                                                                                        121 ISBISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
                                                                                                                                                                    DAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240
                                                                                                                                                                                                            encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a
                                                                                 1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCHSGGGGGSSGGGGANVANVVTDAFFN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to chitinase polypeptides and the polynucleotides
                                                                      SMONCGCOPIVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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                                Length 250;
                                                   4; Indels
                              Score 1372; DB 8;
Pred. No. 2.4e-112;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 68; 197pp; English.
                                                                                                                                                                                                                                                                                                                ADS92684 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                             Chitinase variant polypeptide #31.
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                              97.4%;
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
                            Query Match
Best Local Similarity 97.2
Matches 243; Conservative
                                                                                                                                                                                                                                         GVDPGPNLTC 250
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          Sequence 250 AA;
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                                                                                                                                                                                                                                                                                                                       SPFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGPAHGGSQVQKREIAAFFAHATHETG
                                                                                                                                                                                                                                                                                                                                                                                                                                          HECYISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RVAQDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARVGYYKQY
                                                                                                                                                                                                                           1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVASVVTG
                                                                                                                                                                                                                                                                                        57 SPFNGIKNQAGSGCEGKNPYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFPAHATHETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 RVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQY
                                                                                                                                                                       SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGG----GGANVASVVTG
                                                                                                                Gaps
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                                                Length 254;
                                                                                                             4; Indels
                                                Score 1366; DB 8;
Pred. No. 8.1e-112;
3; Mismatches 4;
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                   97.0%;
95.7%;
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                                                Query Match
Best Local Similarity 95.7°
Matches 243; Conservative
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Sequence 254 AA;
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(VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                Query Match 96.6%;
Best Local Similarity 96.0%;
Matches 240; Conservative
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                                                                               Sequence 250 AA;
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                                                                                                                                                                                                                                                                                    ISEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRDIGFDGLGDPGRVAR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                       DAVVAFKAALWFMMNVHRVMPQFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL
                                                                                                                                                                                1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
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                                                                                                                                             Gaps
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plant resistance to a fungus or nematode. This sequence represents chitinase variant polypeptide of the invention.
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                                                                                                 Length 250;
                                                                                                                                         5; Indels
                                                                                                 Score 1363; DB 8;
Pred. No. 1.5e-111;
5; Mismatches 5;
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14-MAR-2003; 2003US-00389432.
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96.0%;
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Best Local Similarity 96.0
Matches 240; Conservative
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                                                                Sequence 250 AA
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             enhancing
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Heterodera. The polynucleotides and polypeptides are useful in enhand plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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Pred. No. 2.7e-111;
3; Mismatches 7;
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fungus is from the genus Pusarium. The nematode is from the genus theterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                              SMONCGCQPINCCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVANVTDAFFN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to chitinase polypeptides and the polynucleotides
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                                                                                                    SMONCGCOPNIVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGSSGGGGANVASVVTGSFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase
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plants with enhanced resistance against a fungus
                                                               Score 1358; DB 8;
Pred. No. 4e-111;
6; Mismatches 5
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PIONEER HI-BRED INT INC.
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                                                                96.4%;
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N-PSDB; ADS92687.
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Best Local Similarity
Matches 239; Conserv
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polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus feteroderar. The polynucleotides and polypoptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase; plant resistance; fungus; nematode; Pusarium; Heterodera;
maize; chitinase B; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                   DB 8;
                                                                                                                                                                                                                Score 1357.5; DB 8;
Pred. No. 4.6e-111;
4; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize chitinase B polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS92618 standard; protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOYCROLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOYCROLGVDPGPNLTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2003; 2003WO-US033588
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2003US-00389432
                                                                                                                                                                                                                   96.4%;
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                                                                                                                                                                                                                                                                       Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    True T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-365417/34
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                    Sequence 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004037194-A2
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CCX SS X LL LL X B X LL X B X LL X B X LL X B X LL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGV 242
cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genue Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a maize chitinase B polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or
                                                                                                                                                                                                                                                                             KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS
                                                                                                                                                                                                                                                                                                                                                                                                               EISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFNGI
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera
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nematode.
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                                                                                                                                                                            Length 248;
                                                                                                                                                                                                                  4; Indels
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plants with enhanced resistance against a fungus or a
                                                                                                                                                                              Score 1351; DB 8;
Pred. No. 1.6e-110;
6; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS92666 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chitinase variant polypeptide #22
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PIONEER HI-BRED INT INC.
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2002US-00290086.
2003US-00389432.
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                                                                                                                                                                            96.0%;
larity 96.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPGPNLTC 250
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                                                                                                                                                                                          al Similarity
238; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPGPNLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADS92665
                                                                                                                                        Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004037194-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VERD-)
                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-)
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymuclectide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polymuclectides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                          ISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR
                                                                                                                                                                                                                                                                                                                   SMONCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN
                                                                                                                                                                                                                                                                                                                                                                                                        GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker.
                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                           Length 250;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                      Score 1351; DB 8;
Pred. No. 1.7e-110;
6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A maize chitinase polypeptide designated ZmCh2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulating its expression in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 281
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                                                                                                                                                                                                                             96.0%;
94.8%;
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                                                                                                                                                                                                                                                                         Matches 237; Conservative
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                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                      Sequence 250 AA;
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                                                                                                                                                                                                                                Query Match
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(AAB18894, AAB18896, AAB18899, and AAB18902-05), and glucosyl hydrolase famiy 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence shuffling
                                                                                                                                                                             KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 122
                                                                                                                                                                                                                     EISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARDA 182
                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                        214 VVAFKAALWFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQMARVGYYRQYCRQLGV 273
                                                                                                                                                                                                KSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQCKREIAAFFAHATHETGHFCYIS 153
                                                                                                                                                                                                                                        EINKSNAYCDPTKROWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARDA 213
                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or
                                                                                                                                                         34 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFNGI
                                                                                                                                                                                                                                                           VVAPKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGV
                                                                                                                                      QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFNGI
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                  ö
                                                                                               Length 281;
                                                                                                                  Indels
                                                                                             Score 1351; DB 3;
Pred. No. 1.9e-110;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yalpani N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; SEQ ID NO 54; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                        ADS92670 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIONEER HI-BRED INT INC
                                                                                             96.0%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0420666P.
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2003US-00389432.
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                238; Conservative
                                                                                                                                                                                                                                                                                                   DPGPNLTC 250
                                                                                                                                                                                                                                                                                                                      DPGPNLTC 281
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N-PSDB; ADS92669.
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                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     variant
                                                                          Sequence 281 AA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISBISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRDIGFDGLGDPGRVAR
nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhanc plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                           8; Length 250;
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                                                                                                                                                                                                                      Score 1350; DB 8;
Pred. No. 2e-110;
8; Mismatches
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Query Match
Best Local Similarity 94.4
Matches 236; Conservative
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                                                                                                                                                                               Sequence 250 AA;
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PGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYK 234
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                                                                                                                                                                                                                                                                  TGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHE 114
                                                                                                                                                                                                                                                                                                                       TCHFCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGD 174
encoding them. A method of enhancing plant resistance to a fungus or nemacode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Fusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
                                                                                                                                                                                                            54
                                                                                                                                                                                                                            1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRPGGGGGGGGGGGGGGGGGGGGANVASVV 60
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                                                                                                                                                      Length 256;
                                                                                                                                                                                 6; Indels
                                                                                                                                                     Score 1349; DB 8;
Pred. No. 2.6e-110;
4; Mismatches 6;
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93.8%;
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14-MAR-2003; 2003US-00389432
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Best Local Similarity
Matches 240; Conserv
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                                                                                                                              Sequence 256 AA;
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           encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus plant is and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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invention relates to chitinase polypeptides and the polynucleotides
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                                                                                                                                                                                                                                                                               GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHBTGHFCY
                                                                                                                                                                                               Gaps
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                                                                                                                                                                Score 1348; DB 8; Length 250;
Pred. No. 3e-110;
7; Mismatches 5; Indels (
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                 Query Match
Best Local Similarity 95.2%;
Matches 238; Conservative
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RVDPGPNLTC 250
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                                                                                                                                          Sequence 250 AA;
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The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.
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Sequence 256 AA;

TGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHVTHE 120 55 TGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHE 114 1 SMONCGCOPNVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGSSGG-----GGANVASVV 54 1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGCGGGGGGGGGGGGGGAVASVV 60 6; Gaps Length 256; 6; Indels 95.7%; Score 1348; DB 8; 93.8%; Pred. No. 3.1e-110; ive 4; Mismatches 6; Query Match
Best Local Similarity 93.8
Matches 240; Conservative 61 8 8 6 8 6 8 6

TGHFRYISEVNKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNGPAGRAIGFDGLGD 180

TGHFCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGD 174

115 121 175 PGRVARDAVVAFKAALMFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYK 234

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Search completed: May 24, 2005, 12:50:20 Job time: 114.905 secs

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                           US-10-692-367-70
                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                     score:
                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                  Run on:
                                                                                                                                                                                                                                Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

;	Description	Sequence 2, Appli	22,	30,	Sequence 5, Appli	9	Sequence 6, Appli	8	8	9	11	11	Sequence 11, Appl	13	Sequence 13, Appl	7, A	7,	'n	7	'n	Sequence 3, Appli	ý,	9	7,	6	6	Sequence 2, Appli	7
SUMMARIES	ID	US-09-522-714-2	US-09-522-714-22	US-09-522-714-30	US-07-791-931-5	US-07-704-288C-6	US-08-379-259-6	US-07-704-288C-8	US-08-379-259-8	US-07-791-931-6	US-08-047-413-11	US-08-229-050-11	US-08-801-563-11	US-08-475-427-13	US-07-842-165-13	US-07-704-288C-7	US-08-379-259-7	US-07-704-288C-3	US-08-093-372-2	379	US-09-534-229C-3	US-08-475-427-6	07-842	US-07-791-931-7	US-07-704-288C-9	US-08-379-259-9	-09-534-229C	US-09-125-891-2
	DB	4	4	4,	m	٦	-	Н	Н	m	ч	m	ო	~	~	Н	н	Н	-	-	4	~	7	m		Н	4	4
	Query Match Length	281	271	183	328	310	310	330	330	310	324	324	324	329	329	314	314	336	336	336	319	302	302	328	318	318	323	328
de	Query	96.0	61.2	48.7	44.6	44.1	44.1	44.1	44.1	44.1	44.0	44.0	44.0	44.0	44.0	42.8	42.8	42.0	42.0	42.0	41.8	41.3	41.3	40.0	39.6	39.6	39.5	38.0
	Score	1351	861	685.5	627.5	621.5	621.5	•	621.5	621	620	620	620	620	620	602.5	602.5	265	592	592	588	581	581	563	557.5	٠	552.5	535.5
	Result No.	1	7	e	4	Ŋ	9	7	60	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

28	535.5	38.0	328	4	US-09-125-891-4	Sequence 4, Appli
59	504.5	35.8	254	ď	US-08-475-427-1	Seguence 1, Appl:
30	504.5	35.8	254	N	US-07-842-165-1	Sequence 1, Appl
31	504.5	35.8	254	m	US-08-448-398-3	Sequence 3, Appli
32	498	35.4	316	m	US-07-791-931-8	φ,
33	490	34.8	284	4	US-09-522-714-24	24,
34	477	33.9	266	н	US-08-812-025-10	
35	477	33.9	266	٣	US-07-791-931-10	Sequence 10, Appl
36	477	33.9	266	m	US-09-138-873A-10	10,
37	462	32.8	405	4	US-09-902-540-11954	119
38	456.5	32.4	271	4	US-09-266-965-141	
39	392	27.8	372	ო	US-07-791-931-4	4,
40	384.5	27.3	252	4	US-09-522-714-20	20
41	378.5	26.9	256	4	US-09-534-229C-1	Sequence 1, Appli
42	377	26.8	259	4	US-09-522-714-18	18
43	371.5	26.4	253	e	US-07-791-931-9	6
44	367.5	26.1	250	Н	US-08-162-475A-4	Sequence 4, Appli
45	366.5	26.0	253	н	US-08-162-475A-5	Sequence 5, Appli
					ALIGNMENTS	
RESULT 1						
US-09-522-714-2	2-714-2	-09-522-714-2				

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KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 VVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 VVAFKAALWFWMNSVHGVVPQGFGATTRAINGALBCGGNNPAQMNARVGYYRQYCRQLGV 273
                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Salmons, Carl R.
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT FILING DATE: 1999-03-10
EARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                             Query Match

96.0%; Score 1351; DB 4; Length 281;
Best Local Similarity 96.0%; Pred. No. 4.6e-113;
Matches 238; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 DPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Zea mays
US-09-522-714-2
Patent No. 6563020
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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RESULT 2 US-09-522-714-22 ; Sequence 22, Application US/09522714

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Sequence 5, Application US/07791931C
Fatent NO. 6133507
GENERAL INFORMATION:
APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin cDNA;
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12;
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
, ORGANISM: Solanum tuberosum
US-07-791-931-5
                                                                                                                                              244 PG 245
                                                                                                                                                                               PG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
LENGTH: 328
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US-07-791-931-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AVVAFKAALWFWMNNVHR--VMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EI-SKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD 181
                                                                                                                                                                                                                                                                                                                                                                                                                     26 QNCGCASGLCCSRFGYCGTGEDYCGAGCQSGPC----DVPETNNASVASIVTPAFFDAL 80
                                                                                                                                                                                                                                                                                                                                                                                                 3 ONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGSSGGGGANVASVVTGSFFNGI 62
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Nasser
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT ILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/125,915
EARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 183
                                                                                                                                                                                                                                                                                                                                                               8;
GENERAL INFORMATION:
SAPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 183;
                                                                                                                                                                                                                                                                                                                           DB 4; Length 271;
                                                                                                                                                                                                                                                                                                                          61.2%; Score 861; DB 4; Length 27:
62.2%; Pred. No. 3e-69;
tive 25; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.7%; Score 685.5; DB 4; Length ilarity 66.5%; Pred. No. 9.3e-54; Conservative 25; Mismatches 33; Indels
                                                                                     FILE REFERENCE: 1100
CURRENY APPLICATION NUMBER: US/09/522,714
CURRENT FILING DATE: 2000-03-10
BARLIER APPLICATION NUMBER: 60/125,915
BARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PSECSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 30, Application US/09522714; Patent No. 6563020; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 LGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 FGVDPGNNLTC 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Zea mays
US-09-522-714-30
                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Zea mays
US-09-522-714-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-522-714-30
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                                                                                                                                                                                                                   SEQ ID NO 22
LENGTH: 271
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 ET------GHFCYISEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 GPCGRAIGVDLIANPDLVATDPVISFKTALWFWMTPQSPKPSCHDVIIGRWNPSSADRAA 262
126 KSNAYCD-PTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARDAVV 184
                                                                                          185 AFKAALWFWMNNVHRVMPQGFGATIRAINGALEC-DGNNPAQMNARIGYYKQYCRQLGVD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 GPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM-----PQ----- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QNCG------CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGGANVASVV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
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Patent No. 5399680
GENERAL INFORMATION
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: ELEMENTS
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 ----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 NRLPGFGVITNIINGGLECGRGTDNRVQDRIGFYRRXCSILGVTPGDNLDC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
44.6%; Score 627.5; DB 3;
Best Local Similarity 43.3%; Pred. No. 2.8e-48;
Matches 126; Conservative 39; Mismatches 79;
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 THET------GHFCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 NYGPAGRDIGFDGLGDPGRVARDAVVAPKAALWFWMN-----NVHRVM----PQ----- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SMONCG------COPNVCCSKFGYCGTTDEYCGDG-COSGPCRSGGGGSSGGGGANVAS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 SAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC---PGGPTPPGGGDLGS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 ----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 ANRLPGFGVITNIÍNGGLECGRGTDSRVQDRÍGFYRRÝCSILGVSFGDNLDC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.1%; Score 621.5; DB 1; Length 3
42.5%; Pred. No. 9.2e-48;
ive 44; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
TITLE OF INVENTION:
TITLE OF INVENTION: BLENENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
NUMBER OF SEQUENCES: 26
MUMBER OF SEQUENCES: 26
MUMBER OF SEQUENCES: 26
MUMBER OF SEQUENCES: 26
MUMBER OF SEQUENCES: 36
M
                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTOMREY/AGENT INPOMATION:
NAME: REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: F91 8899
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1970RMATION:
TELEPRAK: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
444 South Flower Street, Suite 2000
ZIP: 90071-2921
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TVPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.5%
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-379-259-6
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JOSTON TO SERVICE SEQUENCE SEQUENCES SEQUENCE SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 NYGPAGRDIGFDGLGDPGRVARDAVVAPKAALWFWMN-----NVHRVM----PQ---- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 THET-----GHPCYISEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 SARQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQS-QC---PGGPTPPGGGDLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGANVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 ----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 ANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

44.1%; Score 621.5; DB 1;
Best Local Similarity 42.5%; Pred. No. 9.2e-48;
Matches 124; Conservative 44; Mismatches 77;
PatentIn Release #1.0, Version #1.25
                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relear, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRANICH/OCKET NUMBER: P31 8899
TELERPHONE: (619) 546-4737
TELEPHONE: (619) 546-4737
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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TOPOLOGY: unk
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PRIOR APPLICATION DATA:
                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 TGSFFNG-IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATH 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                      44.1%; Score 621.5; DB 1; Length 330; 43.0%; Pred. No. 9.9e-48; tive 39; Mismatches 80; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 8 Application US/08379259 | Patent No. 5695939 | GENERAL INFORMATION: APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: TITLE OF INVENTION: DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: STREET: 444 South Flower Street, Suite 2000 CITY: LOS Angeles STATE: California CONNTROW. MINISTER CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: REflex, Stephen E.
REGISTRATION NUMBER: 31,192
TREDECOMMUNICATION INFORMATION:
TELEFONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
FILING DATE:
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: E
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.0%
Matches 125; Conservative
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90071-2921
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM-----PQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 NRLPGFGVITNIINGGLECGRGTDNRVQDRIGFYRRYCSILGVTPGDNLDC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 ----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                      Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%; Score 621; DB 3; Length 310; 42.0%; Pred. No. 1e-47; ive 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
44.1%; Score 621.5; DB 1
Best Local Similarity 43.0%; Pred. No. 9.9e-48;
Matches 125; Conservative 39; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6, Application US/07791931C; Patent No. 6133507; GENERAL INFORMATION: APPLICANT: Raikhel, Natasha V.; TITLE OF INVENTION: Nettle Lectin cDNA; FILE REFERENCE: MSU 4.1-114; CURRENT APPLICATION UNDER: US/07/791,931C; CURRENT FILING DATE: 1991-11-12; NUMBER OF SEQ ID NOS: 19; SOFTWARE: PatentIn Ver. 2.0
  US 07/704,288
APPLICATION NUMBER: US 07/704,2 PILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION UNMBER: P31 88
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    (619) 546-4737
                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
                                                                                                                                                               TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Nicotiana tabacum
US-07-791-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-379-259-8
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Best Local Similarity
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159 NYGPAGRDIGFDGLGDPGRVARDAVVAFYAALWFWMNN-------VHRVMPQ---- 203
IISSSMFDQMLKHRNDNACQGKGFYSYNAFINAARSFPGFGTSGDTTARKREIAAFFAQT 123
                                    THET------GHPCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNY 158
                                                                                                                                                                                                                                                                                                                                                                                                      Melchers, Leo S.

Meulenhoff, Elisabeth J.S.

Van Roekel, Jeon S.C.

Sela-Buurlage, Marianne B.

Vloemans, Alexandra A.

Woloshuk, Charles P.

Bol, John F.

Linthorst, Hubertus J.M.

VENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR

VENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                          204 -----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                243 AANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%; Score 620; DB 1; Length 324; 42.0%; Pred. No. 1.3e-47; ive 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
CLASSIFICATION NUMBER: US/08/047,413
FILING APPLICATION 800
PRIOR APPLICATION 1800
PRIOR APPLICATION NUMBER: US 07/647,831
ATPONENT/AGENT INPORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1875-494-0792
                                                                                                                                                                                                                                                                                                                                                                                      Cornelissen, Bernardus J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         US-08-047-413-11
; Sequence 11, Application US/08047413
Patent No. 5670706
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: FUNC
TITLE OF INVENTION: OBTA
TITLE OF INVENTION: POLY
NUMBER OF SEQUENCES: 17
CORRESSONDENCE ADDRESS:
ADDRESSEE: MOITISON &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT:
APPLICANT:
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SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGANVAS 52

Matches 123; Conservative

48;

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197 NYGPCGRAIGVDLINNPDLVATDPVISFKSALWFWMTPQSPKPSCHDVIIGRWQPSSADR 256
                                                                                                                                                                                                  159 NYGPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMNN-------VHRVMPQ---- 203
                                                        53 VVTGSFFNG-IKNQAGSGCEGKNFYTRSAFLSAVKAYPGPAHGGSQVQGKREIAAFFAHA 111
Melchers, Leo S.
Mellenhoff, Elisabeth J.S.
Van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
Bol, John F.
Linthorst, Hubertus J.M.
VENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
                                                                                                                                112 THBT-----GHFCYISBISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNY
                                                                                                                                                                                                                                                                                               204 -----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24615-20022.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cornelissen, Bernardus J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Morrison & Foerster 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08229050
Patent No. 6066491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIPICATION: 800
PRIOR APPLICATION BOOD
PRIOR APPLICATION NUMBER: US 07/647,
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MITCABLIGG, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 29,959
TELECPHONE: 415-813-5600
TELECPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 324 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 755 Page
CITY: Palo Alto
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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LENGTH:
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                                                                                                                                                                                                                                       VVTGSFFNG-IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHA 111
                                                                                                                                                                                                                                                                                           159 NYGPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMNN-------VHRVMPQ--- 203
                                                                      SMONCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGANVAS 52
                                                                                           APPLICANT: Van Roekel, Jeroen S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Wloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Bolyang Fengal Resistant Plants AND RECOMBINANT TITLE OF INVENTION: OPLANTIC FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                              204 -----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                   48;
44.0%; Score 620; DB 3; Length 324; 42.0%; Pred. No. 1.3e-47; ive 43; Mismatches 79; IndelB 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24615-20022.00
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PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/047,413
FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MULESHARE, 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornelissen, Bernardus J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08801563
Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: CORNELISBEN, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIE: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 Query Match
Best Local Similarity 42.0
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                    112 THET----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-801-563-11
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APPLICANT:
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APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
                                                                                                                                                                                                                                                                                                                                                                                                                     112 THET------GHFCYISEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 NYGPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMNN------VHRVMPQ---- 203
                                                                                                                                                                                                                                                                                                                                                                                             53 VVTGSFFNG-IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHA 111
                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                1 SMONCG------CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGGANVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                  48;
                                                                                                                                                                           Query Match
44.0%; Score 620; DB 3; Length 324;
Best Local Similarity 42.0%; Pred. No. 1.3e-47;
Matches 123; Conservative 43; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION NUMBER: FR 90 09460
APPLICATION NUMBER: FR 90 09460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/564/BEDL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-475-427-13
; Sequence 13, Application US/08475427
Setent No. 5859340
; GENERAL INFORMATION:
                     : 324 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington, D.C.
SEQUENCE CHARACTERISTICS
                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                             US-08-801-563-11
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55 TGSPFNG-IKNQAGSGCEGK-NFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 HET-----GHF----CYISEISKSNAYCDPTKROWPCAAGOKYYGRGPLQISWNYN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 YGPCGRAIGVDLIANNPDLVATDPVISFKTAIWFWMTPQSPKPSCHDVIIGRWNPSAGDRS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 YGPAGRDIGFDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM-----PQ----- 203
                                                                                                                                                                                                                                                                                                                                                25 QNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQS-QCPGGGPGPGPVTGGDLGSVI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squence T. Application US/07704288C

| Salent No. 5399680
| GENERAL INFORMATION:
| APPLICANT: LAMB, CHRISTOPHER J.
| APPLICANT: LAMB, CHRISTOPHER J.
| TITLE OF INVENTION: BLEMENTS
| TITLE OF INVENTION: BLEMENTS
| NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: FRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
| CITY: Los Angeles
| STREET: California Communey. Indicated Communey. Indicated Communey. Indicated Communey.
                                                                                                                                                                                                                                                                                                                    3 QNCG-----CQPNVCCSKFGYCGTTDBYCGDG-CQSGPCRSGGGGSSGGGGANVASVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 ANRIPGFGVITNIINGGLECGRGNDNRVQDRIGFYRRYCGILGVSPGDNLDC 314
                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                    Query Match 44.0%; Score 620; DB 2; Length 329; Best Local Similarity 43.8%; Pred. No. 1.3e-47; Matches 128; Conservative 39; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Stephen E.
REGISCHATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 546-4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                      LENGTH: 329 amino acida TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-842-165-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United ZIP: 90071-2921
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Sequence 13, Application US/07842165

Patent No. 593269

GENERAL INFORMATION:

APPLICANT: DUBGIS, Michel

APPLICANT: DUBGIS, Michel

APPLICANT: DUBGIS, Michel

APPLICANT: DIGGIAN; Alain

TITLE OF INVENTION: Recombinant gene coding for a protein

TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: FOLEY & LARDNER

STREET: King Street Station, Suite 500, 1800 Diagonal

STREET: King Street Station, Suite 500, 1800 Diagonal

STREET: WORK OF BOX 299

CITY: ALEXANDRIA

STREET: WIGHTIA

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 YGPCGRAIGVDLLNNPDLVATDPVISFKTAIWFWMTPQSPKPSCHDVIIGRWNPSAGDRS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TGSFFNG-IKNQAGSGCEGK-NFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 HET-----GHF----CYISEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 YGPAGRDIGPDGLGDPGRVARDAVVAFKAALWFWMN-----NVHRVM-----PQ---- 203
                                                                                                                                                                                                                                                                                                                                                               3 QNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGSSGGGANVASVV 54
                                                                                                                                                                                                                                                                                                                                                                                           25 QNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQS-QCPGGGGPGPGPUTGGDLGSVI 83
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 ANRLPGFGVITNIINGGLECGRGNDNRVQDRIGFYRRYCGILGVSPGDNLDC 314
                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                               Query Match

44.0%; Score 620; DB 2; Length 329;
Best Local Similarity 43.8%; Pred. No. 1.3e-47;
Matches 128; Conservative 39; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D ..
REGISTRATION NUMBER: 18,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1876-9300
TELEPAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
(202) 672-5300
(202) 672-5399
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
  TELEPHONE:
                                                                                                                                                                                                               US-08-475-427-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-842-165-13
                      TELEFAX:
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                                                                           Gaps
                                     Query Match 42.8%; Score 602.5; DB 1; Length 314; Best Local Similarity 43.6%; Pred. No. 4.7e-46; Matches 122; Conservative 38; Mismatches 77; Indels 43;
                                                                                                                                                                                                                                   ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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Search completed: May 24, 2005, 12:56:21 Job time : 31.572 secs

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Appl 4, Appl 6, Appl 6, Appl 6, Appl 6, Appl 84, Appl 12, Appl 18, Appl 18, Appl 18, Appl 20, Appl 21, Appl 22, Appl 24, Appl 27, Appl 8, Appl 27, Appl 8, Appl 26, Appl 27, Appl 8, Appl 27, Appl 8, Appl 26, Appl 27, Appl 8, Appl 27, Appl 8, Appl 71, Appl 63, Appl 71, Appl 71, Appl 71, Appl

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Perfect score:

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OTHER INFORMATION: Variant sequence produced by shuffling techniques
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US-10-692-367-70

Sequence 70, Application US/10692367

Publication No. US2005005055A1

GENERAL INFORMATION:

APPLICANT: Miller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Alpani, Nasser

TITLE OF INVENTION: NOVel compositions with chitinase

TITLE OF INVENTION: Activity

TITLE OF INVENTION: NOVEL COMPOSITIONS WITH APPLICANTON NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/399,432

PRIOR FILING DATE: 2003-03-14

PRIOR PLING DATE: 2002-11-06

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PRILING DATE: 2001-11-07

PRIOR PRILING DATE: 2001-11-07

PRIOR PRILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 70

LENGTH: 250

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              24, 2005, 12:54:28; Search time 89.2505 Seconds (without alignments) 936.991 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
ITITE OF INVENTION: Novel compositions with chitinase
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ITITE OF INVENTION: Novel compositions with chitinase
ITITE OF INVENTION: NOVEL COMPOSITION OF STATE 
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Publication No. US20050050595A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
ITILE OF INVENTION: activity
TILE OF INVENTION: activity
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                                                                                                                                                                                                                                               Sequence 82, Application US/10692367
Publication No. US20050050595A1
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241 GVDPGPNLTC 250
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                                            1 SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52, Application US/10692367

Publication No. US2005005055A1

GENERAL INFORMATION:

APPLICANT: Miller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Alpani, Nasser

TITLE OF INVENTION: activity

TITLE OF INVENTION: activity

FILE REFERENCE: 54916200320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/389,432

PRIOR FILING DATE: 2003-10-22

PRIOR FILING DATE: 2003-11-07

PRIOR FILING DATE: 2002-11-06

PRIOR FILING DATE: 2002-11-06

PRIOR FILING DATE: 2002-11-06

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-06

SROTHARER FILING DATE: 2002-11-06

PRIOR FILING DATE: 2002-11-07

SROTHARER: FEASTER FOR WINDOWS Version 4.0

SEQ ID NO 52

LENGTH: 250
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ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 78, Application US/10692367

Publication No. US20050050595A1

GENERAL INFORMATION:
APPLICANT: Miller, Mathias L.
APPLICANT: Simmons, Carl R.
FILE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 10/290,086
PRIOR PILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR PILING DATE: 2000-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 250
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT FILING DATE: 2003-10-22
FRIOR APPLICATION NUMBER: 10/389,432
PRIOR APPLICATION NUMBER: 10/290,086
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2001-11-07
SOFTWARE: PESECTION NUMBER: 60/420,666
PRIOR PILING DATE: 2001-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PESECTION WINDOWS VERSION 4.0
SEQ ID NO 68
LENGTH: 254
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; OTHER INFORMATION: Variant sequence produced by shuffling techniques US-10-692-367-78
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                                                                                                  Length 250;
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Best Local Similarity 96.0%; Pred. No. 5.5e-106;
Matches 240; Conservative 3; Mismatches 7; Indels 0
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Sequence 56, Application US/10692367

Publication No. US2080050595A1

GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Novel compositions with chitinase TITLE OF INVENTION: activity

FILE REFERENCE: 549162000320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT APPLICATION NUMBER: 10/389,432

PRIOR FILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-11-06

PRIOR FILING DATE: 2003-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/307,029

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/300,666

PRIOR FILING DATE: 2001-11-07

PRIOR PLING DATE: 2001-11-07

SEQ ID NOS: 84

SEQ ID NOS: 84

LENGTH: 250
                                                                                              Query Match 96.8%; Score 1363; DB 17; Best Local Similarity 96.0%; Pred. No. 3.1e-106; Matches 240; Conservative 5; Mismatches 5;
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DAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240
                                                                             61 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKRBIAAFFAHATHETGHFCY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-44
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                                                                                                                                                                                                                                                                     US-10-92-36'-44

Sequence 44, Application US/10692367

Publication No. US20050050581

GENERAL INFORMATION

APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

CURRENT APPLICATION NUMBER: 10/290, 086

PRIOR FILING DATE: 2003-11-06

PRIOR FILING DATE: 2003-11-06

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-07

PRIOR FILING DATE: 2002-11-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 250
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                                                                                                                                                             GVDPGPNLTC 250
                                                                                                                                      241 GVDPGPNLTC 250
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RESULT 8 US-10-692-367-72

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54 VTGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATH 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 DPGRVARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYY 233
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Publication No. US20050050581

GENERAL INFORMATION:

APPLICANT: Muller, Mathias L.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: activity

TITLE OF INVENTION: activity

FILE REPERENCE: 549162000220

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-314

PRIOR PELING DATE: 2003-314

PRIOR FILING DATE: 2003-11-06
                                                                          GENERAL INFORMATION

JAPPLICANT: MILIET, MARINAS L.

APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: activity

FILE OF INVENTION: activity

FILE REFERENCE: 549162000320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-22

PRIOR PILING DATE: 2003-03-14

PRIOR PLING DATE: 2002-11-06

PRIOR PLING DATE: 2002-11-06

PRIOR PLING DATE: 2001-11-07

SEQ ID NO 72

LENGTH: 257
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Sequence 72, Application US/106
Publication No. US20050050595A1
GENERAL INFORMATION:
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                                           1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGVVASIVTGSFFN
                                                                                                                                                                                                                                                 121 ISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR
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                                                                                                                              GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY
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Publication No. US20030101484A1

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
ITILE OF INVENTION: Malze Chitinases and Their Use in
ITILE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100D
CURRENT APPLICATION NUMBER: US/10/304,928
CURRENT PILING DATE: 2002-11-26
PRIOR APPLICATION UNMBER: 09/522,714
PRIOR APPLICATION NUMBER: 09/522,714
PRIOR APPLICATION NUMBER: 06/125,915
PRIOR APPLICATION NUMBER: 06/125,915
PRIOR APPLICATION NUMBER: 05/125,915
SPIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 281
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Pred. No. 3.5e-105;
6; Mismatches 4; Indels 0;
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Best Local Similarity 96.0%;
Matches 238; Conservative
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US-10-304-928-2
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US-10-692-367-54
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US-10-692-367-50
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APPLICANT: Muller, Mathias L.
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: True, Thom
APPLICANT: Yalpani, Nasser
ITILE OF INVENTION: Novel compositions with chitinase
ITILE OF INVENTION: NOVER: 2003-0-22
PRIOR APPLICATION NUMBER: 10/389,432
PRIOR APPLICATION NUMBER: 10/290,086
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-06
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 20
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR FILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 248
TYPE: PRT
TYPE: PRT
US-10-692-367-2
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10S-10-692-367-50
Sequence 50, Application US/10692367
Publication No. US20050059581
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.8
Matches 237; Conservative
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61 IDSFFNGIKSQAGSGCEGKNPYTRSAFLSAVKAYPGPAHGGSQVQGKRIAAFPAHVTHE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 TGHFCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 PGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SMONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGG-----GGANVASVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Variant sequence produced by shuffling techniques US-10-692-367-22
                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Variant sequence produced by shuffling techniques US-10-692-367-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.7%; Score 1348; DB 17; Length 250; 95.2%; Pred. No. 5.5e-105; ive 7; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                               Length 256;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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JAPLICANT: Muthler, Mathias L.

APPLICANT: True, Thom

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Alpani, Nasser

TITLE OF INVENTION: activity

FILE REFERENCE: 549162000320

CURRENT FILING DATE: 2003-10-22

PRIOR APPLICATION NUMBER: 10/389,432

PRIOR APPLICATION NUMBER: 10/290,086

PRIOR APPLICATION NUMBER: 10/290,086

PRIOR APPLICATION NUMBER: 60/337,029

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-12-05

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 22

LENGTH: 250
                                                                                                                                                                                                                                                                                                                               95.8%; Score 1349; DB 17;
93.8%; Pred. No. 4.7e-105;
live 4; Mismatches 6;
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10692367; Publication No. US20050050595A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 QYCRQLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYCRQLGVDPGPNLTC 256
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.8%
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 238; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGSSGGGGANVASVVTGSFFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9%; Score 1350; DB 17; Length 250; 94.4%; Pred. No. 3.8e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                         APPLICANT: Muller, Mathias L.
APPLICANT: Muller, Mathias L.
APPLICANT: Miller, Mathias L.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Activity
FILE OF INVENTION: Activity
FILE REFERENCE: 549162000320,
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 10/289,432
PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,029
PRIOR FILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/420,666
PRIOR PILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54

LENGTH. 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MALIEY, Mathias L.
APPLICANT: True, Thom
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Novel compositions with chitinase;
TITLE OF INVENTION: activity
FILE REFERENCE: 549162000320
CURRENT APPLICATION NUMBER: US/10/692,367
CURRENT APPLICATION NUMBER: 10/389,432
PRIOR PILING DATE: 2003-10-27
PRIOR PILING DATE: 2003-10-14
PRIOR PILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-11-06
PRIOR FILING DATE: 2003-11-06
PRIOR PILING DATE: 2002-11-06
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Publication No. US20050050595A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
          Publication No. US20050050595A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 236; Conservative
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61 GIKSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCY 120
                                                                                                                                                                       ISEISKSNAYCDPTKROWPCAAGOKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
                                                                                                                                                                                                121 ISEINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVAR 180
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                                                                                 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAFFAHATHETGHFCY 120
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SMONCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN 60
                        SMQNCGCASGLCCSRFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SMQNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGG-----GGANVASVV 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.7%; Score 1348; DB 17; Length 256; 93.8%; Pred. No. 5.7e-105; Live 4; Mismatches 6; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NESULT 15

Sequence 48, Application US/10692367

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Novel compositions with chitinase

TITLE OF INVENTION: Activity

FILE REFERENCE: 549162000320

CURRENT APPLICATION NUMBER: US/10/692,367

CURRENT FILING DATE: 2003-10-14

PRIOR PILING DATE: 2003-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/420,666

PRIOR PILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 48
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Matches 240; Conservative
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241 RVDPGPNLTC 250
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Search completed: May 24, 2005, 13:12:28 Job time : 90.2505 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 24, 2005, 12:39:31 ; Search time 24.6548 Seconds (without alignments) 975.638 Million cell updates/sec

US-10-692-367-70 1408 Perfect score:

1 SMONCGCOPNVCCSKFGYCG......GYYKQYCRQLGVDPGPNLTC 250 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descri	chitinase (EC 3:2.	(EC 3	chitinase (EC 3.2.	'n	5	chitinase (EC 3.2.	probable endochiti	chitinase (EC 3.2.	chitinase class 4	probable chitinase	probable endochiti	•	chitinase (EC 3.2.	O	probable chitinase	a	(EC 3	e (EC 3	probable endochiti	probable endochiti	ð		chitinase class IV		chitinase (EC 3.2.	chitinase (EC 3.2.	(EC 3.	chitinase (EC 3.2.	chitinase (EC 3.2.
SUMMARIES	۵	B42424	A42424	\$25311	S51678	T47601	S46536	A84868	S16579	S57476	T03405	H84867	T09131	T14345	T14348	T14341	T14344	A44039	JE0125	G84867	C84868	D84868	S51645	865778	T09687	S05426	S20981	S56694	T03614	S08627
	DB	2	~	~	N	7	~	~	7	7	7	~	~	~	7	~	~	-	7	~	7	~	~	N	~	٦	N	~	N	7
	f Query Match Length	268	280	268	261	273	288	264	270	249	229	265	276	266	266	268	268	250	208	277	281	283	247	266	327	328	324	324	323	329
	Query Match	93.4	89.9	62.0	61.0	59.3	58.9	58.9	58.5	57.2	57.0	56.0	55.6	54.5	54.5	54.1	53.6	52.8	52.1	50.9	50.6	49.3	49.1	48.5	45.4	44.6	44.1	44.0	43.4	43.4
		1314.5	1265.5	873	859	834.5	829.5	829	823.5	805	802.5	788.5	783	768	167	762	754	744	733.5	717	712.5	693.5	691.5	682.5	639	627.5	621	619.5	611.5	611.5
		-	7	e	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

chitinase (EC 3.2.			chitinase (EC 3.2.		chitinase (EC 3.2.				probable chitinase		chitinase (EC 3.2.	chitinase (EC 3.2.		chitinase class 1	probable chitinase
JC2071	843317	865020	865019	S20982	S37344	838670	S15997	B45511	T04403	S59953	T06999	T07000	T07838	S57482	T04484
~	7	~	~	7	-1	7	~	~	~	~	~	~	~	~	~
302	318	316	318	334	322	320	336	335	318	322	329	329	311	321	332
43.2	43.2	43.0	43.0	42.8	42.4	42.2	42.0	41.4	41.4	41.2	41.2	41.0	41.0	40.4	40.2
608.5	608.5	605.5	605.5	602	597.5	594.5	592	583.5	583	580.5	580.5	577.5	577	269	266
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B42424 chitinase (EC 3.2.1.14) precursor - maize (fragment) C;Species: Zea mays (maize) C;Species: 12-Mar-1993 #sequence_revision 03-Feb-1994 #text_change 10-Jul-1998 C;Accession: B42424
 R;Huynh, Q.K.; Hironaka, C.M.; Levine, B.B.; Smith, C.B.; Borgmeyer, J.R.; Shah, D.M. J. Biol. Chem. 267, 6635-6640, 1992 A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifunga A;Reference number: A42424; MUID:92202208; PMID:1551872
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-268 <huy> A;Cross-references: GB:M84165 A;Cross-references: GB:M84165</huy>
A;Note: Une authorist Liminatoru Liminatoru (1978) on 101 Lesique 197 as man, vo. 101 Lesique 197 as 0 on 116, CAA for residue 231 as Asn and CGC for residue 232 as Gly C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl C;Keywords glycosidase; hydrolase; polysaccharide degradation F;20-55/Domain: hevein chitin-binding domain homology <hcb> F;20-55/Domain: plant chitinase homology <pch></pch></hcb>

Gaps 1; DB 2; Length 268; Score 1314.5; DB 2; Length Pred. No. 1.4e-95; 6; Mismatches 9; Indels 93.4%; Matches 233; Conservative Similarity Query Match Best Local S

62 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYI 121 80 IKNQAGSGCEGKNFYTRSAFLSAVKGYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYI 139 122 SEISKSNAYCDPTXRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGPDGLGDPGRVARD 181 61 20 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGRGGGGGGANVASVVTSSFFNG 79 3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSG-GGGSSGGGGANVASVVTGSFFNG 242 VDPGPNLTC 250 g 8 8 셤 g ò 8 ò ò

VDPGPNLTC 268 260 RESULT 2

A42424 chithnase (EC 3.2.1.14) A - maize C.Species: Zea mays (maize) C.Spate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-1999

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chitinase (EC 3.2.1.14) class I -
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Matches 153; Conservative
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                                                                              Matches 153; Conservative
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                                                  Similarity
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C;Accession: A4244; A42260

R;Huynh, Q.K.; Hironaka, C.M.; Levine, B.B.; Smith, C.B.; Borgmeyer, J.R.; Shah, D.M.
J. Biol. Chem. 267, 6455-640; 1992

A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifunga A;Reference number: A42424; MUID:92202208; PMID:1551872

A;Reference number: A4244

A;Reference number: A4244; MUID:92202208; PMID:1551872

A;Reducule type: mRNA

A;Residues: 1-280 acHUy-

A;Rolecule type: mRNA

A;Residues: 1-280 acHUy-

A;Note: sequence extracted from NCBI backbone (NCBIN:89874, NCBIP:89876)

A;Note: sequence extracted from NCBI backbone (NCBIN:89874, NCBIP:89876)

R;Verburg, J.G.; Smith, C.E.; Lisek, C.A.; Huynh, Q.K.
J. Biol. Chem. 267, 3886-3893, 1992

A;Note: sequence extracted from NCBI backbone (NCBIN:89874, NCBIP:89876)

R;Verburg, J.G.; Smith, C.E.; Lisek, C.A.; Huynh, Q.K.
J. Biol. Chem. 267, 3886-3893, 1992

A;Title: Identification of an essential tyrosine residue in the catalytic site of a chit oppil)- carbodismide.

A;Reference number: A42260; MUID:92156129; PMID:1740436

A;Rocession: A42260

A;Roces
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525311
childranese (EC 3.2.1.14) precursor - rape
C;Species: Brassica napus (rape)
C;Decies: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C;Accession: S25311
R;Rasmussen, U; Bojsen, K.; Collinge, D.B.
Plant Mol. Biol. 20, 277-287, 1992
A;Title: Cloning and characterization of a pathogen-induced chitinase in Brassica napus.
A;Reference number: S25311; MUID:93004480; PMID:1391771
A;Resference: S25311; MUID:93004480; PMID:1391771
A;Residues: 1-268 -RAS>
A;Cross-references: UNIPROT:Q06209; EMBL:X61488; NID:917798; PIDN:CAA43708.1; PID:917795
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; PI C;Reywords: glycosidase; hydrolase; polysaccharide degradation
C;Reywords: glycosidase; hydrolase; polysaccharide degradation
C;Reywords: glycosidase; hydrolase; poredicted <SIG>P;22-869/Domain: signal sequence #status predicted <SIG>P;25-869/Domain: hevein chitinase #status predicted <MAT>P;74-268/Domain: plant chitinase homology <PCH>P;74-268/Domain: plant chitinase homology <PCH</p>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRVARDAVVAPKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQ 235
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89.9%; Score 1265.5; DB 2; Length
Best Local Similarity 86.7%; Pred. No. 9.7e-92;
Matches 221; Conservative 13; Mismatches 14; Indels
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A;Accession: S51678
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:Q43150; EMBL:Z46948; NID:g603881; PIDN:CAA87072.1; PID:g6038
A;Cross-references: UNIPROT:Q41150; EMBL:Z46948; NID:g603881; PIDN:CAA87072.1; PID:g6038
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;16-51/Domain: hevein chitin-binding domain homology <HCB>
F;61-261/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 PTVAFRTGLWFWMNSVRPVLNQGFGATIRAING-MECNGGNSGAVNARIRYYRDYCGQLG 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 RDAVVAFKAALWFWMNNVHR--VMPQGFGATITRAINGALECDGNNPAQMNARIGYYKQYC 237
                                                                                                                                                                                                                                                                                                                                         BIS-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-Jul-2004
                                                                                                                                              1 SMONCGCOPINYCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGSSGGGGANVASVVTGSFFN
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                                                                                                              3 QNCGCQPNVCCSKPGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSPPNGI
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Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 261;
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                                4.3e-61;
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60.5%; Pred. No. 5.2e-60;
ive 31; Mismatches 61
     DB 2;
                                                       33; Mismatches
     62.0%; Score 873;
                                Pred. No.
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C,Accession: A84868
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Ko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 216579
R;Margis-Pinheiro, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.; Burkard Plant Mol. Biol. 17, 243-253, 1991
A;Title: Isolation of a complementary DNA encoding the bean PR4 chitinase: an acidic enz
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C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
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                                                                                                                                                    167
                                                                                                                                                                                                                                                                                      GFDGLGDPGRVARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMN 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable endochitinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
   146 ISHETTNLCHIEERDGDVGDAYCDQDKAAQYPCAAGKKYYGRGPLQLSWNYNYALAGQAI
                                                                                                                                                                                                                                                                                                                              GFDGLGNPEKVATDVNTSFKAAMWFWMTNVHSVMNQGFGATTKAINGALECNGQNQDQAN
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                                                                                                                                                ATHETGHFCYISEI--SKSNAYCDPTK-ROWPCAAGOKYYGRGPLOISWNYNYGPAGRDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                228 ARIGYYKOYCROLGVDPGPNLTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :||:|| || || || || DRIQFYKKYCADFGVAPGDNLTC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 VDPGPNLTC 250
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A;Molecule type: DNA
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S46556
chitimes (EC 3.2.1.14) - beet
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Accession: S46536
R;Nielsen, K.K.; Bojsen, K.; Roepstorff, P.; Mikkelsen, J.D.
Plant Mol. Biol. 25, 241-257, 1994
A;Title: A hydroxyproline-containing class IV chitinase of sugar beet is glycosylated wing R;Reference number: S46536; MUD:94289648; PMID:8018873
A;Accession: S46536
A;Status: preliminary
A;Molecule: type: mRNA
A;Residues: 1-288 ANIE>
A;Cross-references: UNIPROT:P42820; EMBL:L25826; NID:9510277; PIDN:AA32916.1; PID:95102
C;Superfamily: lectin-related plant chitinase; hevein chitinase; hevein chitinase; polygaaccharide degradation
F;28-64/Domain: hevein chitinase homology <PCH>
class IV chitinase (CHIV) - Arabidopsis thaliana
N;Alcernate names: protein T12E18.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47601
R;Blocecker, H., i Newes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24469
A;Reference number: Z24469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 < SHC)
A;Residues: 1-273 < SHC)
A;Residues: cultivar Columbia; BAC clone T12E18
C;Genetics:
A;Map position: 3
A;Introns: 139/1
A;Note: T12E18.110
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 QNCGCSSELCCSQFGFCGNTSDYCGVGCQQGPCFA---PPPANGVSVAEIVTQEFFNGI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNCGCQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGS------SGGGGANV 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.3%; Score 834.5; DB 2 60.2%; Pred. No. 4.4e-58; ive 23; Mismatches 71
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Best Local Similarity 59.34
Matches 156; Conservative
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Best Local Similarity 60.2
Matches 150; Conservative
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A;Accession: T03405
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Experiments: 1-229 <TRU>A;Cross-references: UNIPROT:004138; EMBL:AB003194
A;Experimental source: cv. Nipponbare
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;30-229/Domain: plant chitinase homology <PCH>
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Map position: 2
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pla
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A;Cross-references: UNIPROT:024598; GB:AE002093; NID:92281112; PIDN:AAB64048.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 FFAHVTHETGHMCYINEINGANMDYCDKSNKQWPCQPGKKYYGRGPLQISWNFNYGPAGK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 GANVASVVTGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 FFAHATHETGHFCYISEISKSNA-YCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGR 165
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C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable endochitinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ONCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chitinase cDNA
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Matches 140; Conservative 27; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiTruong, N.; Itoh, Y. submitted to the EmBL Data Library, April 1997 A;Description: Nucleotide sequence of rice class II A;Reference number: 214936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.0%; Score 802.5;
                                                                                                                                                                                                                                                                                                                 probable chitinase (EC 3.2.1.14) IIb - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNARIGYYKQYCRQLGVDPGPNLTC 250
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Olgvdtgdnltc
             239 QLGVDPGPNLTC
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A;Molecule type: DNA
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                                                                                              238
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A;Reference number: S16579; MUID:91322521; PMID:1863776
A;Accession: S16579
A;Accession: RNA
A;Molecule type: mRNA
A;Residues: 1-270 «MAR»
A;Cross-references: UNIPROT:P27054; EMBL:X57187
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Superfamily: lectin-related plant chitinase; polysaccharide degradation
F;24-59/Domain: hevein chitin-binding domain homology «HCB»
F;70-270/Domain: plant chitinase homology «PCH»
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S17476
chitinase class 4 - cowpea (fragment)
c;Species: Vigna unguiculata (cowpea)
c;Species: 10-Oct-1958 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: 557476
R;Vo, L.T.T. Broughton, W.; Krause, A.
C;Accession: 55746
A;Accession: 55746
A;Accession: 55746
A;Accession: 55746
A;Accession: 57476
A;Accession: breliminary
A;Accession: Complexion 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YISEI-SKSNAYCDPTK-RQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDAVVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAQNCGCAEGLCCSQYGYCGTGEDYCGTGCQQGPCTTASPPPSN----NVNADILTADFL 77
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59.5%; Pred. No. 8.2e-56;
iive 27; Mismatches 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; Score 823.5; DB 2
59.7%; Pred. No. 3.2e-57;
ive 28; Mismatches 67
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A; Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosamn A; Pathway: polysaccharide degradation C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;21-56/Domain: hevein chitin-binding domain homology <HCB>
F;69-266/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami A; Pathway: polysaccharide degradation C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl C; Keywords: glycosidase; hydrolase; polysaccharide degradation F; 21-56/Domain: hevein chitin-binding domain homology <PGP>
F; 21-56/Domain: plant chitinase homology <PGP>
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                                                                                                                              A;Cross-references: UNIPROT:Q96410; EMBL:U52847; NID:g1549332; PID:g1549333 A;Experimental source: strain sg766 trophy C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-266 <KRA>
A;Cross-references: UNIPROT:Q96411; EMBL:U52848; NID:g1549334; PID:g1549335
A;Experimental source: strain sg766 trophy
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable chitinase (EC 3.2.1.14) EP3B/E6, class IV - carrot
C;Species: Daucus carota (carrot)
C;Date: 20-58p-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGPAHGGSQVQGKREIAAFFAHATHETGHFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 SAQNCNCAAGLCCSKHGYCGTTSDYCGEGCQAGPC-TNTAPTGGGNGVSVADIVTDDFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIISQATGDCDGKNFYTRSAFLNALQSYSSFGTSGSADDSKREIAAFFAHATHETGYFCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ISEIS-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGSSGGGGANVASVVTGSFFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 768; DB 2;
; Pred. No. 6.8e-53;
38; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 767; DB 2;
; Pred. No. 8.1e-53;
35; Mismatches 72
                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-266 <KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T14348
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
Submitted to the EMBL Data Library, March 1996 A;Reference number: 217995 A;Accession: T14345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T14348
R;Kragh, K.; De Vries, S.C.
Romitted to the EMBL Data Library, March 1996
A;Reference number: 217995
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Best Local Similarity 55.4%,
Matches 139; Conservative
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Best Local Similarity 55.8*
Matches 140; Conservative
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C; Species: Picea glauca (white spruce)
C; Species: Picea glauca (white spruce)
C; Species: Picea glauca (white spruce)
C; Species: Discassion: 1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C; Accession: T09131
R; Dong, J. Z.; Dunstan, D.I.
Submitted to the EMBL Data Library, January 1996
A; Description: Developmental regulation of a gene encoding chitinase during somatic embrances: University; translated from GB/EMBL/DDBJ
A; Reference number: Z16579
A; Reference number: Z16579
A; Molecule type: mRMA
A; Residues: 1-276 < DON
A; Cross-references: UNIPROT:Q40838; EMBL:L42467; NID:g1161164; PID:g1161165
C; Genetics:
A; Gene: Chi
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology +HCB>
F; 27-62/Domain: hevein chitin-binding domain homology +HCB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 PVVAPRTALWFWMKSVRPVLNQGFGATIRAISG-FDCDGRNLGGVNARIGYYRDYCGQLG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 122
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                                                                      KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHFTGHFCYIS 122
                                                                                                                                                              RIS-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD 181
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chitinase (EC 3.2.1.14) EP3-3/E7, class IV - carrot
C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14345
R;Kragh, K.; De Vries, S.C.
VVAPKAALWFWM--NNVHRVMP--QGFGATIRAINGALECDGNNPAQMNARIGYYKQYCR
                                                                                                                                                                                                                                                        AVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 2;
4.7e-54;
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Matches 135, Conservative
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LDPGANITC 265
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probable chitinase (EC 3.2.1.14) EP3-1/H5, class IV - carrot (fragment)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14341
R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; K Plant Mol. Biol. 31, 631-645, 1996
A;Title: Characterization of carrot chitinases able to rescue the temperature-sensitive
A;Reference number: Z17992; MUID:96382431; PMID:8790295
A;Reference number: Z17992; MUID:96382431; PMID:8790295
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary;
A;Molecule type: mRNA
A;Residues: 1-268 eKRA.
A;Residues: 1-268 eKRA.
A;Experimental source: strain 89766 trophy
C;Genetics:
A;Mote: EP3
C;Function:
A;Pethway: polysaccharide degradation
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                           180 RDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQ 239
                                                                                                                                                                                                                                                                                                        197 SDAVVSFKTALMYWKVKVQSVTSQGFGATIRAIN-SIECNGGSPDAVNSRVSLYNSYCSK 255
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                                                                                                                                                                                121 ISEIS-KSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVA 179
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19 SAQNCNCTAGLCCSKHGYCGTTSDYCGEGCQAGPC-TNTAPTGGGGNGVSVADIVTDDFFN 77
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                                                                                                                                                                                                                                                                                                                                                                                                                         FGVAPGDNQRC 266
                                                                                                                                                                                                                                                                                                                                                                               240 LGVDPGPNLTC 250
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Best Local Similarity
Matches 139; Conserv
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Search completed: May 24, 2005, 12:55:13 Job time : 25.6548 secs Q6jbk7 zea mays (8 Q6jbl3 zea mays (8 P29022 zea mays (m Q94el5 saccharum o Q6jbl6 tripsacum d Q94el3 sorghum bal Q93vt2 sorghum bic Q93vt1 sorghum bic Q93vt1 sorghum bic Q94el4 sorghum aru Q7y1z0 oryza sativ Q7xu64 oryza sativ Q7xu64 oryza sativ Q7xu64 oryza sativ

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

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Result Š.

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63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Pubmed=15280246; DOI=10.1534/genetics.104.026856; Tiffin P., "Comparative evolutionary histories of chitinase genes in the genus
                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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I Genetics 167:1331-1340(2004).

R EMBL; AY532735; AAT90004.1; ...

R EMBL; AY532735; AAT9992.1; ...

R EMBL; AY532735; AAT9992.1; ...

R EMBL; AY532735; AAT9992.1; ...

R GO; GO:0008604; F:chitin binding; IEA.

R GO; GO:0004568; F:chitin binding; IEA.

R GO; GO:0006032; P:chitin catabolism; IEA.

R GO; GO:0006032; P:chitin catabolism; IEA.

R GO; GO:0006032; P:chitin catabolism; IEA.

R GO; GO:0006032; P:chitin binding 1.

R InterPro; IPR001002; Chitin binding 1.

R InterPro; IPR00102; Chitin binding 1.

R PEAN; PR0012; Glyco_hydro_19.

R PEAN; PR00182; Glyco_hydro_19.

R PEAN; PR00182; GHYCO_19.

R PEAN; PR00182; GHYCO_19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 AA; 28925 MW; 8F38B91DE3B48BE6 CRC64;
                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodon; PD000609; Chittin binding 1; 1.
Prodon; PD354900; Chittin binding 1; 1.
Prodon; PD354900; Chibi.
Prodon; PD354900; Chibi.
PROSITE; PS00070; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
PROSITE; PS000773; CHITINASE 19 1; 1.
PROSITE; PS000774; CHITINASE 19 2; 1.
PROSITE; PS00026; CHIT BIND 1 1; 1.
Chitin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1351; DB 2;
Pred. No. 4.7e-102;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                    279 AA
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060BK7
060BL3
CHGA MAIZE
094EL5
094EL3
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094L15
094EL4
07Y1Z0
07XU64
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ilarity 96.0%;
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                               89.4
886.9
883.0
880.2
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nes 238;
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Name=chiB;
1263.5
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- 2005 Compugen Ltd
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Gapop 10.0 , Gapext 0.5
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212 AVVAPKAALWFWINSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQYCRQLG 271
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                                                                                        182 AVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLG
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"Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
EMBL; AY532729; ART39998.1; -.
HSSP; P10969; 1K7V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 0008568; F: chitin binding; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

R GO; GO: 00016599; P: cell wall catabolism; IEA.

R GO; GO: 0009613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IRR001002; Chitin binding_1.

R InterPro; IRR001002; Chitin binding_1.

R PRIMTS; PR001451; GHITMENIDNG.

R PRODOM; PD554900; Glyco hydro_19; 1.

R PRODOM; PD554900; Glyco hydro_19; 1.

R PROSTITE; PS00669; Chitin binding_1; 1.

R PROSTITE; PS00773; CHITMENED DEHYDR CLU; UNKNOWN_1.

R PROSTITE; PS00773; CHITMASE_19: 1.

R PROSTITE; PS00774; CHITMASE_19: 1.
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SEQUENCE 283 AA; 29405 MW; 551581E126791A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLOME TROW N.A. PubMed=15280246; DOI=10.1534/genetics.104.026856;
                                                                                                                                                                                                                                                                                                                                                                                                                     283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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62 IKNOAGSGCEGKNPYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYI 121
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                                                                                                                         EINKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARDA
                                                                                                                                                                                                                                          3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGGSSGGGGANVASVVTGSFFNG
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                                                                                           EISKSNAYCDPTKROWPCAAGOKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARDA
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Wararyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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EMBL, AYS32733, AAT40002.1; --.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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Best Local Similarity 96.0
Matches 239; Conservative
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Name=chiB;
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272 YCRQLGVDPGPNLTC 286
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                                                                                                                                                          Name=chiB;
                                                                                                                                              Chitinase
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                                                                             Q6JBP7
Q6JBP7;
                                                     RESULT 5
Q6JBP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 GHFCYISEINKSNAYCDPSKROWPCAAGOKYYGRGPLOISWNYNYGPAGRAIGFDGLGDP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 GRVARDAVVAFKAALWFWANSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQ 271
              274
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3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGG-----SSGGGGANVASVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHET
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                                                                                                                                                                                                                                                                                                                                          "Comparative evolutionary histories of chitinase genes in the genus
                                                                                                                                                                                                                      Zea diploperennis (Diploperennial teosinte).
Zea diploperennis (Diploperennial teosinte).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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R GO; GO: 0008568; F: chitin binding; IEA.

R GO; GO: 00016598; P: chitinase activity; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

R GO; GO: 000613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IRR001002; Chitin binding_1.

R InterPro; IRR001002; Glyco_hydro_19.

R PRINTS; RR00451; GHTINBINDNG.

R PRODOM; PD154900; Glyco_hydro_19; 1.

R PRINTS; RR00451; CHITINBINDNG.

R PRODOM; PD154900; Glyco_hydro_19; 1.

R RARY; SW00270; Chellin_binding_1; 1.

R RRARY; SW00270; Chellin_binding_1; 1.

R RROSITE; PS000687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.

R PROSITE; PS00026; CHITINBIND_1; 1.

R PROSITE; PS00026; CHITINBIND_1; 1.
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Chitin-binding.
centrace 286 AA; 29352 MW; 7577FPEE94C0773A CRC64;
                                                                                                                                                      (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
                                                                                                                                  286 AA
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Genetics 167:1331-1340(2004).
BEBL; AYS32740; AAT40009.1; -
HSSP; P10969; 1K7V.
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                                                                                                                                 PRELIMINARY;
                                        VDPGPNLTC 250
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275 VDPGPNLTC 283
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                                                                                                                                                                                                 Chitinase.
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"Comparative evolutionary histories of chitinase genes in the genus are and family poacese.";

"Comparative evolutionary histories of chitinase genes in the genus are and family poacese.";

"Genetics 167:1331-1340(2004).

"RMBL; AY532736; AAT40005.1; -..

"RMSL; AY532736; AAT4005.1; -..

"RMSL; AY532736; AAT4006.1; -..

"RMSL; AY53770; AAT4006.1; -..

"RMSL; AY54706.1; -..

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Skaryotei, Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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95.6%; Pred. No. 7e-101;
ive 6; Mismatches 4; Indels
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PROSITE; PS00773; CHITINASE 19 1; 1.
PROSITE; PS00774; CHITINASE 19 2; 1.
PROSITE; PS00726; CHIT_BIND_I 1; 1.
PROSITE; PS50941; CHIT_BIND_I 2; 1.
CRITIN-binding.
CRITIN-binding.
278 AA; 28838 MW; RD65AB2FCED91585 CRC64;
                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
278 AA
PRT;
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Matches 237; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||||||
DPGPNLTC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPGPNLTC 250
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243 DPGPNLTC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P10969; 1X7V
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4576;
05-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
                                                                                                                                                     Name=chiB;
                                                                                                          Chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ო
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Q6JBP5
   SON SERVICE STREET STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCYISEISKSNAYCDPTKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARDAVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARDAVVAFKAALWFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQMNARVGYYRQYC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGSSSSGGGGANVASVVTGS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCYISEINKSNAYCDPSKRQWPCAAGGKYYGRGPLQISWNYNYGPAGKAIGFDGLGDPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGG-----SSGGGGANVASVVTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
EMBL; AYS37724; AAT39993.1; --.
HSSP; P10969; 1K7V.
                                                                                                                                                                                                                                                                                                                                  Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A GO; GO: 0008061; F: chitin binding; IEA.

R GO; GO: 0004568; F: chitin binding; IEA.

R GO; GO: 0004568; F: chitinase activity; IEA.

R GO; GO: 00016998; P: cell wall catabolism; IEA.

R GO; GO: 0006913; P: response to pest, pathogen or parasite; IEA.

R InterPro; IRR001202; Chitin binding 1.

R InterPro; IRR001205; Glyco_hydro_19.

R PERMYS; PR00142; Glyco_hydro_19.

R ProDom; PD154900; Glyco_hydro_19; 1.

R PRODOM; PD154900; Glyco_hydro_19; 1.

R PROSTIE; PS00069; Chitin binding_1; 1.

R PROSTIE; PS00773; CHITINENDED

R PROSTIE; PS00773; CHITINENED

R PROSTIE; PS00774; CHITINENED

R PROSTIE; PS00775; CHITINED

R PROSTIE; PS00775; CHITINENED

R PROSTIE; PS007
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SEOUENCE 284 AA; 29256 MW; B210EB7C204A6567 CRC64;
                                                                                                                                         (TrEMBLrel. 27, Created) (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.9%; Score 1336.5; DB 2
93.7%; Pred. No. 7.2e-101;
iive 7; Mismatches 4;
                                                                          284 AA
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Best Local Similarity 93.7
Matches 237; Conservative
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=76912;
                                                                                                                                                                                 05-JUL-2004
05-JUL-2004
                                                                                                                                                     05-JUL-2004
                                                                                                                                                                                                                                                                   Chitinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
                                                                          Q6JBQ9
RESULT 6
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A PARTE SERVICE SERVIC

278 AA

PRT;

PRELIMINARY;

Q6JBP2 Q6JBP2;

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91 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYIS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 VVAFKAALWFWMNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLGV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRDIGFDGLGDPGRVARDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 ONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRS-GGGSSGGGGANVASVVTGSFFNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSGGGGANVASVVTGSFFNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
EMBL; AY532741; AAT40010.1; -.
                                                                                                                                                          Zea diploperennis (Diploperennial teosinte).
Wakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R GO; GO: 0008668; F: chitin binding; IEA.

R GO; GO: 0008568; F: chitin binding; IEA.

R GO; GO: 00016598; F: chitinase activity; IEA.

R GO; GO: 00016598; P: cell wall catabolism; IEA.

GO; GO: 0006139; P: cell wall catabolism; IEA.

R GO; GO: 0009613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IRR001029; Chitin binding_1.

R InterPro; IRR001025; Glyco_hydro_19.

R Propom; PRO0182; Glyco_hydro_19.

R Probom; PD544900; Glyco_hydro_19; 1.

R PROSTTS; PRO0609; Chitin binding_1; 1.

R PROSTTS; PRO0609; ChitIn BIND_1; 1.

R PROSTTS; PRO0773; CHITINASE_19_1; 1.

R PROSTTS; PRO0773; CHITINASE_19_1; 1.

R PROSTTS; PRO0773; CHITINASE_19_1; 1.

R PROSTTS; PROOF CHITINASE_19_1; 1.

R PROSTTS; PROOF CHITINASE_19_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0941; CHIT_BIND_I_2; 1.
Chitin-binding.
SEQUENCE 278 AA; 28865 MW; 23A117EDFABBF908 CRC64;
(TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ġ
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Best Local Similarity 95.6'
Matches 237; Conservative
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05-JUL-2004
05-JUL-2004
25-OCT-2004
Chitinase.
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EMBL; A HSSP; F GO; GO: EMBL;

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92 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVOGKREIAAFFAHATHETGHFCVI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 ONCGCÓPNYCCSKFGYCGTTDEYCGDGCÓSGPCRSGGGGSSGGSSGANVASVVTGSFFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 SEINKSNAYCDPSKRQWPCAAGGKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 AVVAFKAALWFWMNNVHRVMPQGFGATIRAINGALECDGNNPAQMNARIGYYKQYCRQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AVVAFKAALWFWMSVHGVVPQGFGATTRAINGALBCGGNNPAQMNARVGYYRQYCRQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 SEISKSNAYCDPTKROWPCAAGOKYYGRGPLOISWNYNYGPAGRDIGFDGLGDPGRVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGGSSGGGGANVASVVTGSFFNG
                                                                                                                                                                Tiffin P.; "Comparative evolutionary histories of chitinase genes in the genus
Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.94; Score 1335.5; DB 2; Length 280; 95.24; Pred. No. 8.5e-101; ive 6; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                  parasite; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitin-binding.
SEOUENCE 280 AA; 29009 MW; 64BB647946D9F05F CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                      SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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                                                                                                                                                                                                                                                                           MSSP; F10959; IX.V.

G0; G0: 0008661; F: chitin binding; IEA.

G0; G0: 0004568; F: chitinase activity; IEA.

G0; G0: 0006599; P: chitin actabolism; IEA.

G0; G0: 0006532; P: chitin catabolism; IEA.

G0; G0: 0009613; P: response to pest, pathogen or InterPro; IRR01002; Chitin binding_1.

InterPro; IRR01002; Chitin binding_1.

InterPro; IRR01002; Chitin binding_1.

PERMIS; PR00451; CHITINBINDNG.

ProDom; PD000609; Chitin binding_1; 1.

PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1 PROSITE; PS00774; CHITINASE 19_2; 1.

PROSITE; PS00774; CHITINASE 19_2; 1.
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                                                                                                                                                                                                   zea and family poaceae.";
Genetics 167.1331-1340(2004).
EMBL; AX532734; AAT40003.1; --
HSSP; P10969; 1K7V.
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272 VDPGPNLTC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                  NCBI_TaxID=76912,
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                             "Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae."; Genetics 167:1331-1340(2004).
                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                           R GO; GO: 000806; F: chitin binding; IEA.

R GO; GO: 0004566; F: chitin binding; IEA.

R GO; GO: 00016998; P: chitinase activity; IEA.

R GO; GO: 00016998; P: chitin catabolism; IEA.

R GO; GO: 0009613; P: response to pest, pathogen or parasite; IEA.

R InterPro; IPR001209; Aldehyd dehydrog.

R InterPro; IPR00120; Chitin binding_1.

R InterPro; IRR000726; Glyco hydro_19; 1.

R PRINTS; PR00451; CHTINBINDNG.

R PRODOM; PD001609; Chitin binding_1; 1.

R PRODOM; PD01609; Chitin binding_1; 1.

R PRODOM; PD010609; Chitin binding_1; 1.

R PRODOM; PD010609; Chitin binding_1; 1.
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Chitin-binding.
centrance 278 AA; 29024 MW; 6DDA23E340CA0610 CRC64;
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Last annotation update)
                                                                                                                                        SEQUENCE PROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PSO0773; CHITINASE 19 1; 1.
PROSITE; PSO0774; CHITINASE 19 2; 1.
PROSITE; PSO0076; CHIT BIND 1 1; 1.
PROSITE; PSO9941; CHIT_BIND 1 2; 1.
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Pred. No. 8.5e-101;
6; Mismatches 4;
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                     diploperennis (Diploperennial
                                                                                                                                                                                                                                                          EMBL; AY532738; AAT40007.1; -. EMBL; AY532739; AAT40008.1; -.
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95.6%;
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Best Local Similarity 95.63
Matches 237; Conservative
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Chitinase.
Name=chiB;
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212 AVVAFKAALWFWMNSVHGVVPQGFGATTRAINGALECGGNNPAQWNARVGYYRQYCRQLG 271
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PubMed=15280246; DOI=10.1534/genetics.104.026856;

Tiffin P.;

"Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae.";
Genetics 167:1331-1340(2004).
                            evolutionary histories of chitinase genes in the genus
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                            R GO; GO: 0008661; F:chitin binding; IEA.

GO; GO: 0008668; F:chitinase activity; IEA.

GO; GO: 0016998; P:cell wall catabolism; IEA.

GO; GO: 0016998; P:cell wall catabolism; IEA.

GO; GO: 0006032; P:chitin catabolism; IEA.

GO; GO: 0000613; P:chitin catabolism; IEA.

GO; GO: 0000613; P:chitin catabolism; IEA.

GO; GO: 0000613; P:chitin Elabora.

R InterPro; IPR001202; Chitin Elabora.

R InterPro; IPR001202; Chitin Elabora.

R PROMIN; PR00412; CHITININDG.

R ProDom; PD00669; Chitin binding 1; 1.

R PROSITE; PS00669; ALDEHYDE DEHYDE GLU; UNKNOWN 1.

R RSMARY; SM00270; ChtBD1; 1.

R ROSITE; PS006773; CHITINASE 19-1; 1.

R ROSITE; PS006773; CHITINASE 19-2; 1.

R PROSITE; PS006874; CHITINASE 19-2; 1.

R RROSITE; PS006874; CHITINASE 19-2; 1.
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(TrEMBLrel. 27, Last annotation update)
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Pred. No. 8.5e-101;
6; Mismatches 5;
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                                                        zea and family poaceae.";
Genetics 167.1331.1340(2004).
EMBL; AY537725; AAT39994.1; --
HSSP; Pl0969; 1K7V.
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Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                            "Comparative evolutionary histories of chitinase genes in the genus
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                               R GO; GO: 0008061; F: chitin binding; IEA.

R GO; GO: 0004568; F: chitin binding; IEA.

R GO; GO: 0004568; F: chitin binding; IEA.

R GO; GO: 0004598; P: cell wall catabolism; IEA.

GO; GO: 0006693; P: cell wall catabolism; IEA.

R InterPo; IPR001002; P: chitin catabolism; IEA.

R InterPo; IPR001002; Chitin Dinding_1.

R InterPo; IPR001002; Glyco_Nydro_19.

R PERMYS; RR00451; CHITINBINDNG.

R Probom; PD006609; Chitin Dinding_1; 1.

R PRINTS; RR00451; CHITINBINDNG.

R Probom; PD154900; Glyco_Nydro_19; 1.

R PROSTIE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.

R PROSTIE; PS000697; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.

R PROSTIE; PS00026; CHIT_BIND_1; 1.

R PROSTIE; PS00026; CHIT_BIND_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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SEOUENCE 280 AA; 28963 MW; 60FA617488839998 CRC64;
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Last annotation update)
                                                 SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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SEQUENCE FROM N.A.
PubMed=15280246; DOI=10.1534/genetics.104.026856;
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Pred. No. 8.5e-101;
5; Mismatches 6;
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                                                                                                                                                                           zea and family poaceae.";
Genetics 167:1331-1340(2004).
EMBL; AY532731; AAT40000.1; --
HSSP; P10969; 1K7V.
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Best Local Similarity 95.2%;
Matches 237; Conservative 5
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NCBI_TaxID=76912;
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                                                                                                                   Tiffin P.;
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RESULT 11

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62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFFAHATHETGHFCYI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 SEISKSNAYCDPTXRQWPCAAGQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD
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Genetics 167:1331-1340(2004).
Genetics 167:1331-1340(2004).
HSSP: P10569; IKTV.
GO; GO:00008661; F:chitin binding; IEA.
GO; GO:00004568; F:chitinase activity; IEA.
GO; GO:0016998; P:cell wall catabolism; IEA.
GO; GO:00006032; P:chitin catabolism; IEA.
GO; GO:0000613; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR002086; Aldehyd_dehydrog.
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Rekaryota viridiplantae; Streptophyta; Babryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
R GO; GO:0016998; P:cell wall catabolism; IRA.
R GO; GO:0006012; P:chitin catabolism; IRA.
GO; GO:0009613; P:response to peat, pathogen or parasite; IEA.
InterPro; IPR001002; Chitin binding_1.
R InterPro; IPR00102; Chitin binding_1.
R PRINTS; PR00125; Glyco_Hydro_19.
R PRINTS; PR0041; GHTINBINDNG.
R Probom; PD006069; Chitin binding_1; 1.
R PROBOT; SN00270; ChtBD1; 1.
R PROSITE; PS006773; CHITINASE 19; 1.
R PROSITE; PS00773; CHITINASE 19; 1.
R PROSITE; PS00773; CHITINASE 19; 1.
R PROSITE; PS00774; CHITINASE 19; 1.
R PROSITE; PS00775; CHITINASE 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.6%; Score 1331.5; DB 2; Length 280; 94.8%; Pred. No. 1.8e-100; ive 6; Mismatches 6; Indels 1;
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poates; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                               R GO; GO:0008061, Ir.V.

R GO; GO:0008568; F:chitin binding; IEA.

R GO; GO:0008568; F:chitinase activity; IEA.

R GO; GO:0006598; P:cell wall catabolism; IEA.

GO; GO:0006092; P:cell wall catabolism; IEA.

R GO; GO:0006012; P:response to pest, pathogen or parasite; IEA.

R InterPro; IRR001002; Chitin Binding 1.

R InterPro; IRR001002; Chitin Binding 1.

R PERMINS; PRO0185; GIYCo. hydro. 19.

R PRIMYS; PRO0185; GIYCo. hydro. 19.

R PRODEM; PD00000; GIYCo. hydro. 19.

R PRODEM; PD00000; GIYCo. hydro. 19.

R PROSITE; PS00087; CHITINENNDNG.

R PROSITE; PS00087; CHITINENNDNG.

R PROSITE; PS00026; CHITINENND EDHYDR. GLU; UNKNOWN. 1.

R PROSITE; PS00026; CHITINEND II.

R PROSITE; PS00041; CHITINEND II.

R PROSITE; PS00041; CHITINEND II.

R Chitin-binding.
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94.8%; Pred. No. 1.5e-100;
tive 7; Mismatches 5; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GO; GO:0004568; F:chitinase activity; IEA.
              EMBL; AY532727; AAT39996.1; -. HSSP; P10969; 1K7V.
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Genetics 167.131-1340(2004).
EMBL: AY532726; AAT39955.1; --
HSSP; P10969; 1K7V.
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Matches 236; Conservative
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T as and family poaceae ";
T as and family poaceae ";
Genetics 167:1331-1340(2004).

EMBL; AYS32722; AAT39991.1; -..

EMBL; AYS37222; AAT39991.1; -..

EMBL; AYS3722; Projectin binding; IEA.

R GO; GO:0008061; F:chitinase activity; IEA.

R GO; GO:0016998; P:cell wall catabolism; IEA.

R HITERPO; IPR001002; Chitin binding 1.

R InterPro; IPR001002; Chitin binding 1.

R InterPro; IPR00126; Glyco_hydro_19.

R PRINTS; PR00451; CHITINBINDNG.
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94.4%; Score 1329.5; DB 2; Length 282;
Best Local Similarity 94.8%; Pred. No. 2.6e-100;
Matches 236; Conservative 5; Mismatches 7; Indels 1;
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Wataryora, Viridiplantee, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PubMed=15280246; DOI=10.1534/genetics.104.026856;
Tiffin P.;
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InterPro; IPR001002; Chitin_binding_1.
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Name=chiB;
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                                                     PROSITE; PSO0667; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PSO0773; CHITINASE 19_1; 1.
PROSITE; PSO0774; CHITINASE 19_2; 1.
PROSITE; PSO0026; CHIT BIND 1 1; 1.
PROSITE; PS50941; CHIT_BIND_1 2; 1.
Chitin-binding.
SEQUENCE 281 AA, 28979 WW; C235237FE12D986A6 C
                                                                                                                                                                                                                                                       Pred. No. 2.9e-100
6; Mismatches 6;
                                                                                                                                                                                                                                          94.4%; Score 1329;
ProDom; PD000609; Chitin binding 1; 1. ProDom; PD354900; Glyco hydro 19; 1. SMART; SM00270; ChtBD1; 1.
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Job time : 113.919 secs
                                                                                                                                                                                                                                                            94.48;
                                                                                                                                                                                                                                                            Best Local Similarity 94.4
Matches 236; Conservative
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Perfect score:

Sequence:

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Scoring table:

Total number

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PAT 17-AUG-2003
AY532737 Zea diplo
AY53273 Zea diplo
AY53272 Zea mays
AY53725 Zea mays
AY53727 Zea mays
AY53272 Zea mays
AY53272 Zea mays
AY53273 Zea mays
AY53278 Zea diplo
AY53278 Zea mays
AY53277 Zea mays
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Simmons, C.R. and Yalpani, N.
Maize chitinases and their use in enhancing disease resistance in
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Patent: US 6563020-A 1 13-MAY-2003;

Location/Qualifiers

1. .1094

/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1 from patent US 6563020.
AR321624
AR321624.1 GI:33706864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                   AY532731
AY532739
AY532734
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AY532728
                                                                                                             AY532724
AY532736
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1351.00
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Unclassified.
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Best Local Similarity:
Query Match:
DB:
  Unknown.
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Pred. No.:
 RESULT 1
AR321624
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
   ORIGIN
                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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M84165 Zea mays ch
AY532735 Zea mays
AY532733 Zea mays
                                                                           ; Search time 2973.37 Seconds
  (without alignments)
  4074.095 Million cell updates/sec
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                                                                                                                                              SMONCGCQPNVCCSKFGYCG......GYYKQYCRQLGVDPGPNLTC
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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MZECHITB
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AY532733
                                                                             23, 2005, 15:37:22
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: gb ba: *

2: gb htg: *

3: gb ow: *

5: gb ow: *

6: gb ph: *

7: gb ph: *

9b pr: *

9b vi: *
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Maximum DB seq length: 2000000000
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1408
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93.4
92.8
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Database :

Score

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1351

1314.5 1312.5 1306.5

us-10-692-367-70.rge

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                       source text: Zea mays (library: Lamda GT 10 corn seed ) seed DNA.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                      Location/Qualifiers
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Zea mays

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (bases 1 to 810)

Huynh, Q.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R.
and Shah, D.M.
Antifungal proteins from plants; Purification, molecular cloning,
and antifungal properties of chitinaees from maize seed
J. Biol. Chem. 267 (10), 6635-6640 (1992)
                                                                                                                                                                             GlulleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
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                                                                                                                              GACGAGTACTIGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGCCAGC 269
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                                                                                                                                                             SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle
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                                           GlnAsnCysGlvCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
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Zea mays chitinase B (seed chitinase) gene, 3'end.
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               US-10-692-367-70 (1-250) x AR321624 (1-1094)
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                                                      LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu
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LtC"
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1121 bp DNA linear PLN 29-JUL-2004
Zea mays subsp. parviglumis isolate p15 chitinase (chiB) gene,
complete cds.
AY532735
AY532735.1 GI:48093251
AlaValValalaPheLysAlaAlaLeuTrpPheTrpMetAsnValHisArgValMet 201
                                                                    CCGCAGGGTTCGGCCCACCACCAGGCCATGCAACGCGCCCTCGAGTGCGGGGGGAAAC 720
                                                                                                       Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota; subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Leases 1 to 1121)
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gorner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. 1121
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/mol type="genomic DNA"
/isolate="pl566688"
/isolate="pl5"
                                                   ProGlnGlyPheGlyAlaThr11eArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn
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Conservative:
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/db_xref="taxon:76912"
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/gene="chiB"
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gene="chiB"
codon atart=1
product="chitinase"
/brotein id="AAT4004.1"
/db_xref="GI:48093252"
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AYS12737
Zea diploperennis isolate d2 chitinase (chiB) gene, complete cds.
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                                                                                                                                                                                                                                                                                                               707 TACGGGCCCGCGGGGAGGGCCATCGGCTTCGACGGGCTCGGGGAGGCCCGGCAGGGTGGCG 766
                                                                                                                                                                                                                                                                                                                                              180 ArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpWetAsnAsnValHisArg 199
                                                                                                                                                                                                                                                                                                                                                                                                                         Zea diploperennis
Zea diploperennis
Eukaryota, Viridlantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Submitted (23-3DA-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                   TyrileSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpPro
                                                                                                                                                                                  TyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAla
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                                                                          467 TCTATTAACCTCGCTCTTCAGCGCGCGCGGGTTCTTTGATTTTTGACCCATCAAGCTGA
                                                                                                         -----PheCyB
                                                                                                                                     527 TCAATTTTTTTTGGAAAATTTTCCGCTGCTGTGTCTGTGTCCACGGGCAGATTTCTGC
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/mol_type="genomic DNA"
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/gene="chiB"
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/gene="chiB"
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      Zea mays subsp. parviglumis
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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                                                                                                                                                      2 (bases 1 to 1127)
Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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                                                                                              Comparative evolutionary histories of chitinase genes in the
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/mol_type="genomic DNA"
/cultivar="M106"
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Matches:
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/db_xref="taxon:76912"
<14. .>982
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/gene="chiB"
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/gene="chiB"
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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Conservative:
Mismatches:
Indels:
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                                            Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 GACGAGTACTGCGGCGACGGGGCCAGTCGGGCCCGTGCCGCTCG---GGCGGCGGCAGC
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Matches:
Conservative:
Mismatches:
Indels:
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Zea diploperennis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
1 (bases 1 to 1081)
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CAGAACTGCGGCTGCCAAACGTCTGCTGCAGCAAGTTCGGCTACTGCGGCACGACC 166
                                                                                                                                                                                                                                                                                                                                  GAGATCGCCGCCTTCTTCGCGCACGCCACGCACGAGACCGGGCGTAAGTTGGCTCGGTCT 463
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                                                                                                                                                                                                                                                                                                 GluileAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis---------
                                  AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer
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Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1127)
Tiffin, P.
Comparative evolutionary histories of chitinase genes in the genus
Zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
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                                                             TyrlyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArg 165
                                                                                                                                      PheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPhe 205
                                                                                                                                                                          GlyAlaThr11eArgAla11eAsnGlyAlaLeuGluCysAepGlyAsnAsnProAlaGln 225
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                           TACTACGGGCGCGGCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGGAGG
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Tiffin,P.
Direct Submission
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/organism="Zea mays subsp. parviglumis"
/mol_type="genomic DNA"
/cultivar="P1384064"
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subsp. parviglumis isolate
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/db_xref="taxon:76912"
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/gene="chiB"
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/product="chitinase"
/protein_id="AAT39992.1"
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clade; Panicoideae; Andropogoneae; Zea.
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167 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGGCGGC
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complete cds.
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Tiffin, P.
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/product="chitinase"
/db_xref="chitinase"
/db_xref="chiti
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AYS32725

AND A linear PLN 29-JUL-2004

AND AND BOD Chilinase (ChiB) gene, Complete cds.

AYS32725

AYS32725.1 GI:48093231
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    GAACAACCCCGCCCAGATGAACGCGCGCGTCGGCTACTACAGGCAGTACTGCCGCCAGCT 946
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 1114)
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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. 1114
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/gene="chiB"
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Genetics 167 (3), 1331-1340 (2004)
12 (bases 1 to 1114)
Tiffin,P.
                                           uGlyValAspFroGlyProAsnLeuThrCys
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linear PLN 29-JUL-2004
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Zea mays subsp. parviglumis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
                                Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
1. 1133
                                                                                                                                                   CGCCGCGGGGCAGAAGTACTACGGCGCGCGCTGCTGCAGATCTCGTGGAACTACAACTA
                                                                                                                                                                                                              rGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAr
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cskroycgtddrycgocgopcrsogogsssogoganuvasuvagsprugiknoagg
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mycdpptkrowpcaaqokyyorgplaiswnynygpaaraigpoglodbgruadavva
praalumpunusuhguvoggpgattraingalegognnpagmarugyyrqycrquod
Tiffin, P.

String Tiffin, P.

Direct Submission

L. Submission

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

1551 Location/Qualifiers

1 . .123

| organism="Zea mays Subsp. parviglumis" |
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KYCDESKRQWPCAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARDAVVAF
KAALMFWMNSVHGVVPQGFGATTRAINGALECGGNNFAQWNARVGYYRQYCRQLGVDP
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Zea mays subsp. parviglumis

Eukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD

clade, Panicoideae, Andropogoneae, Zea.

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Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="P1384061"
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    Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
                                                                   1. .1128
/organism="Zea diploperennis"
/moltype="genomic DNA"
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<14. .>995
                                                                                                                                                                                                                            /gene="chiB"
join(<14. .470,592. .>995)
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                                                                                                                                                                                                                                                                                           /product="chitinase"
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/db_xref="GI:48093262"
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complete cds.
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                                                                                                                CTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCGCAGGGGGAGGGCAAG
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                                            286
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                                                                                                                                                                               LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
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sceae; PACCAD
       61
| IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe
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Zea diploperennis isolate d6 chitinase (chiB) gene,
AY532740
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Genetics 167 (3), 1331-1340 (2004)
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Zea diploperennis
Bukaryota; Viridiplantae;
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Tiffin, P.
Direct Submission
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                                                                                                                                                                                                    227 GGCGGCAGTGGCGGCGGTGGGAGCGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAAC 286
                                                                                                                                                              107 CAGAACTGCGGCTGCCAGCCAAACGTCTGCTGCAGCAAGTTCGGCTACTGCGGCACGACC
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Matches:
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| Jan xxef="T418093246"
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                                                                                                                                                                                                                                                                                                                1126 bp DNA linear PLN 29-JUL-2004
Zea maye subsp. parviglumis isolate pl1 chitinase (chiB) gene,
Complete cds.
AY532732
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Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                  rTrpAsnTyrAsnTyrG1yProAlaG1yArgAsp1leG1yPheAspG1yLeuG1yAspPr
                                                              CGGCAGGGTGGCGCGGGGACGCCGTTCGAAGGCGGCGCTTCTGGTTCTGGATGAA
                                                                                                                                                  nAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comparative evolutionary histories of chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sub_species="parviglumis"
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Genetics 167 (3), 1331-1340 (2004)
15280246
2 (bases 1 to 1126)
Tiffin,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="chitinase"
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SNAYCDPSKRQWPCAAGQKYYGRGPLQISWNYNYGPAGKAIGFDGLGDPGRVARDAVU
AFKAALMFWMNSVHGVVPQGFGATTRAINGALBCGGNNPAQMNARVGYYRQYCRQLGV
DPGPNLTC"
                          1138 bp DNA linear PLN 29-JUL-2004 subsp. parviglumis isolate p3 chitinase (chiB) gene,
                                                                                                                                                                                                        genna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGGCAGCAGCAGCAGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTGGCTCGTCACCGGCTCC 286
                                                                                                     Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
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                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly---
                                                                                                                                                                                                   Comparative evolutionary histories of chitinase genes in the
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Matches:
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join(14. .464,589. .992)
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/db_xref="taxon:76912"
<14. .>992
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        78 ArgSerAlaPheLeuSerAlaValLyBAlaTyrProGlyPheAlaHisGlyGlySerGln
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        347 CGGAGCGCGTTCCTGAGCGCCGTCCAGGCTTCGCCCATGCCGAGGTCGCAG
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                                                                                                                                                                         AAGCTGGCTCTATTAACCTCGCTCTTCAGCGCGCGCGCAGGTTCTTTGATTTTTGAC
                                                                                                                                                                                                                                                                                     117 His-PheCysTyrIleSerGlulleSerIysSerAsnAlaTyrCysAspProThrLysAr
                                                                                                                                                                                                                                                                                                                                               gGlnTxpProCysAlaAlaGlyGlnLysTyxTyxGlyArgGlyProLeuGlnIleSerTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 uGluCysAspGlyAspAspProAlaGlnMetAspAlaArgIleGlyTyrLysGlnTy
                                                                                                                                                                                                                                                          527 CCATCATGCTGATCATTTTTTTTGGAAAATTTTCCGCTGCTGTGTCTGTGTGCACGGGC
                                                                                                                                                                                                                                                                                                                 587 AGATITICIGCIACAICAGCGAGAICAACAAGAGCAACGCCIACIGCGACCCGAGCAAGAG
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Ad892671 Chitinase
Ad892669 Chitinase
Ad892669 Chitinase
Ad892637 Chitinase
Ad892637 Chitinase
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Ad892637 Chitinase
Ad892647 Chitinase
Ad892647 Chitinase
Ad892649 Chitinase
Ad892647 Chitinase
Ad892647 Chitinase
Ad892651 Chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             True I, Simmons CR, Yalpani N;
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                                                                                                                                                                                                                                                                      ADS92661
ADS92679
ADS92647
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ADS92657
ADS92623
ADJ12126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VERD-) VERDIA INC. (PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2003; 2003WO-US033588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS92685 standard; DNA; 753
  WO2004037194-A2.
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    Command line parameters:

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-MODEL=frame+_p2n.model -DEV=x1h
-G=/CQm1_1/USPTO spool/USIO6921867/runat 20052005 172254 19994/app query.fasta_1.846
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-MODE=LOCAL -OUTFWTT=pto -NOFM=ext -HEAPSIZE=500 -MININEN=0 -WAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ads22685 Chitinase
Ads2267 Chitinase
Ads2263 Chitinase
Ads2263 Chitinase
Ads2263 Chitinase
                                                                                          ; Search time 370.316 Seconds (without alignments) 3996.417 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                         1 SMONCGCOPNVCCSKFGYCG......GYYKQYCRQLGVDPGPNLTC 250
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                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    4390206 seqs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
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ADS92667
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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97.4
97.0
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Database :

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601 ATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCGACGGG 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
                                  221 AsnAsnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyrCysArgGlnLeu
                                                                   661 AACAACCCCGCCCAGATGAACGCGCGTTCGGCTACTACAAGCAGTACTGCCGCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerMetGlnAsnCysGlyCysGlnProAsnValCysCysScrLysPheGlyTyrCysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                                                                                                         ds; plant resistance; fungus; nematode; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 753 BP; 135 A; 245 C; 265 G; 108 T; 0 U; 0 Other;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                      The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The Hugus is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCGCAGGTGCAGGGG
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                                                                                                                                                                                                 New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 81; 197pp; English
                                                                           Muller ML, True T, Simmons CR,
VERDIA INC.
PIONEER HI-BRED INT INC
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1372.00
98.40%
97.20%
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US-10-692-367-70 (1-250) x ADS92683 (1-765)
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AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu
                                                                                       AACAACCCCGCCCAGATGAACGCGCGCATACTACTACAAGCAGTACTGCCGCCAGCTC
                                 Met ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly
                                            New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                      Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
Heterodera.
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                                                                                                                    GlyValAspProGlyProAsnLeuThrCys 250
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                                                                                                                                                                                                                                                 Chitinase variant polynucleotide #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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P-PSDB; ADS92684.
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Pred. No.:
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Length:
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Conservative:
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3.16e-113 1366.00 96.85% 95.67% 97.02%

Percent Similarity: Best Local Similarity: Query Match: DB:

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                                                                                                                                                                                                                                                                                                                          GlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrp
                                                                                                     41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerValValThrGly
                                                                                                                                                                     77 ThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySer
                                                                                                                                                                                                                      GlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGly
                                                                                                                                                                                                                                                                                                                                                                                         421 CAGTGGCCGTGCGCCGCGGGCAGAAGTACTACGGGCGCGCCCGCTGCAGATCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                         481 AACTACAACTACGGGCCCGGGGGGGGCCCATCGGCTTCGACGGGCTCGGGGACCCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyr
                                                                                                                                                       57 SerPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyr
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22-OCT-2003; 2003WO-US033588
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                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase; gene;
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                                                                                                                                                                                                                                                           The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
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                                                                                                                                                                                          New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 753 BP; 142 A; 244 C; 262 G; 105 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 77; 197pp; English.
                                                                                                                        Muller ML, True T, Simmons CR,
                                                                                (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC.
                         22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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98.00%
96.00%
22-OCT-2003; 2003WO-US033588
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P-PSDB; ADS92694.
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Best Local Similarity:
Query Match:
DB:
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541 GACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAGCGTGCACGTGTG
                                                                                                                                                                                                                                                                                                     221 AsnAsnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyrCysArgGlnLeu
                                                                                                                                                                                                                                                                                                                                     MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly
                                                                                                                                                                                                                                AspalavalvalalapheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; plant resistance; fungus; nematode; Fusarium;
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                            US-10-692-367-70 (1-250) x ADS92671
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                                                                                                                                                                                                                                                                                                                                                                   New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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14-MAR-2003; 2003US-00389432.
22-OCT-2003; 2003WO-US033588
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P-PSDB; ADS92660.
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Sequence 774 BP; 142 A; 249 C; 278
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                                                                                                                                                     AsnasnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyrCysArgGlnLeu
         MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly
                                                                                                                                                                           GlyProAlaGlyArgAspileGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg
                                                           AspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal
                                                                                               GACGCCGTGGTGCGTTCAAGGCGGCGCTCTGGTTCTGGAACAACGTGCACCGTGTG
                                                                                                                                     New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
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                                                                                                            141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                        AsnAsnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyrCysArgGlnLeu
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                                     121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys
                                                            ATCAGCGAGATCAGCAAGAGCAACGCCTACTGCGACCCGACCAAGAGGCAGTGGCGTGC
                                                                                                                                                                                  GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgYalAlaArg
                                                                                                                                                                                                                                                                              601 GCGCCGCAGGGGTTCGGCGCCACCATCAGGGCCATCAACGGCGCACTCGAGTGCGGGG
                                                                                                                                                421 GCCGCGGGGGGAAGTACTACGGGCGCGCCGCTGCAGATCTCGTGGAACTACAACTAC
                                                                                                                                                                                                                        481 GGGCCCGCGGGGGAGGGCCATCGGCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGCG
                                                                                                                                                                                                                                                        AspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal
                                                                                                                                                                                                                                                                                                                                  201 Met ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitinase, glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New maize chitinase genes encoding seven chitinases of glucosyl hydro family 19 are useful for enhancing disease resistance in crop plants modulating its expression in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a maize chitinase polypeptide designated ZmCh2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GlyValAspProGlyProAsnLeuThrCys 250
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P-PSDB; AAB18894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to chitinase polypeptides and the polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                          New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                      ds; plant resistance; fungus; nematode; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 753 BP; 138 A; 238 C; 270 G; 107 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                 Simmons CR,
                                                                                                                                                                                                                                                                                          (VERD-) VERDIA INC.
(PION-) PIONEER HI-BRED INT INC
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2002US-00290086.
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06-NOV-2002;
14-MAR-2003;
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Pred. No.:
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                    Chitinase;
Heterodera.
                                                                         Synthetic
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AAB18899, and AAB18902-05), and glucosyl hydrolase famiy 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynuclectides are also useful as molecular markers for genotype in a plant, and for sequence shuffling.
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                                                                                                                                                                         GlnAanCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
                                                                                                                                                                                                                AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer
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                                                          Sequence 1094 BP; 226 A; 339 C; 368 G; 161 T; 0 U; 0 Other;
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                                                                              ds; plant resistance; fungus; nematode; Pusarium;
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                                       Chitinase variant polynucleotide #24
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(PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
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02-DEC-2004 (first entry)
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                                  11eSerGlulleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys
                                                              AlaalaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr
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The invention relates to chitinase polypeptides and the polymucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polymucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Rusarium. The nematode is from the genus Heterodera. The polymucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polymucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaalaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspalavalvalalaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal
                                                                                                                                                                                                     T; 0 U; 0 Other;
                                                                                                                                                                                                                                                            753
238
7
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                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                     Sequence 753 BP; 132 A; 247 C; 269 G; 105
                                                                                                                                                                                                                                                                                                                                                               Gaps:
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74

300 114

94

420

134

480 174

154

900 214

540 194 720

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us-10-692-367-70.rng

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215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArg1leGlyTyrTyrLys 234
                                         TTCTACACCCGGAGCGCGTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGC
                                                                                                                                                                                  GlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu
                                                                                                                                                                                                                                                                     115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThr
                                                                                                                                                                                                                                                                                             361 ACCGGGCATTTCCGCTACATCAGCGAGGTCAACAAGAGCAACGCCTACTGCGACCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                    SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 CCCGGCAGGCTGGCGCGGGACGCCTGGTTCAAGGCGCGCCCTCTGGTTCTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                 481 TCGTGGAACTACAACTACGGGCCCGCGGGGGGGCCATCGGCTTTGACGGGCTCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 AACAACGTGCACCGTGTGATGCCGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGC
                     ThrGlySerPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsn
                                                                                                    75 PheTyrThrArgSerAlaPheLeuSerAlaValLyBAlaTyrProGlyPheAlaHisGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yalpani N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase variant polymucleotide #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-365417/34.
P-PSDB; ADS92690.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinase; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004037194-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding them. A method of enhancing plant resistance to a fungus or nemacode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Pusarium. The nematode is from the genus plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly '20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to chitinase polypeptides and the polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                                                 Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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CGCGTCGACCCAGGCCCCAACCTCACCTGC 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 47; 197pp; English.
                                                                                                                                                                                                        Chitinase variant polynucleotide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmons CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2002; 2002US-0420666P.
06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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1348.00
95.31%
93.75%
95.74%
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                                                                              ADS92663 standard; DNA; 771
                                                                                                                                                                 (first entry)
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P-PSDB; ADS92664.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                        WO2004037194-A2
                                                                                                                                                                 02-DEC-2004
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                                                                                                                                                                                                                                                                     Heterodera
                                                                                                                                                                                                                                                                                                              Synthetic.
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The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or mematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
                        New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                   Claim 4; SEQ ID NO 73; 197pp; English.
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Sequence 771 BP; 140 A; 249 C; 275 G; 107 T; 0 U; 0 Other;

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ACCGACTCCTTCTTCAACGCATCAAGAGCCAGGCCGGGAGCGGGTGCGAGGAACAAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlySerGlnValGlnGlyLygArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 194
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Matches:
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encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Pusarium. The nematode is from the genus Heterodera. The plant polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.
                                                                                                                                                                                                                     ds; plant resistance; fungus; nematode; Fusarium;
                                                    721 CAGTACTGCCGCCAGCTCGGCGTCGACCCAGGCCCAACCTCGC
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                                        GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                             Chitinase variant polynucleotide
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(PION-) PIONEER HI-BRED INT INC.
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06-NOV-2002; 2002US-00290086.
14-MAR-2003; 2003US-00389432.
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Best Local Similarity:
Query Match:
DB:
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Search completed: May 23, 2005, 17:44:57 Job time : 374.316 secs

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Run on:

US-10-692-367-70

Perfect score:

Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

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GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Sequence 37, A Sequence 37, Sequence 37, Sequence 37, Sequence 31, Sequence 29, Sequence 15, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 20, Assequence 20, Assequence 20, Assequence 20, Assequence 20, As
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Sequence 9, A
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APPLICANT: Simmons, Nasser
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Maize Chitinases Resistance in Crop Plants
FILE REPERENCE: 1100
CURRENT PILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/125,915
EARLIER APPLICATION NUMBER: 60/125,915
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PRSEUSE FOR WINDOWS Version 3.0
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US-08-971-217-37

US-09-9156-234-37

US-09-916-234-37

US-09-522-714-21

US-09-522-714-21

US-08-229-050-10

US-08-229-050-10

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US-08-448-398-6

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; Sequence 1, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
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-DBV TIMBOUT=120 -WARN TINEOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                            ; Search time 125.74 Seconds (without alignments): " " 3253.303 Million cell updates/sec
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1 SMQNCGCQPNVCCSKFGYCG......GYYKQYCRQLGVDFGPNLTC 250
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-522-714-1

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US-08-444-803-37

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US-08-446-37

US-08-456-265A-37

US-08-456-265A-37

US-08-456-416-37

US-08-457-344-37

US-08-457-344-37

US-08-457-348-37
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1351 861 830 830 830 830 830 830 830

Length

Query Match

Result

Database :

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Searched:

Appl Applia Appl

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117 CAGAACTGCGGGTGGGCGTCGGGCCTGTGCTGCAGCCGGTTCGGGTACTGCGGGGAGACGGGC 176
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                                                          Length:
Matches:
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                                                         1.9e-84
861.00
72.11%
62.15%
61.15%
; LOCATION: (42)...(854)
US-09-522-714-21
                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-181-271A-37
                                             Alignment Scores:
Pred. No.:
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                                                                                                                       AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCACCGGCTCCTTCTTCAACGGCATC
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Sequence 21, Application US/09522714

Patent No. 6563020

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Malze Chitinases and Their Use in TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants FILE REPERENCE: 1100

CURRENT APPLICATION NUMBER: US/09/522,714

CURRENT PILING DATE: 2000-03-10

BARLIER APPLICATION NUMBER: 60/125,915

BARLIER PILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspProGlyProAsnLeuThrCys 250
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FEATURE:
NAME/KEY: CDS
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APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                  APPLICANT: Williams, Shericca C.
IIILE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
IIILE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION PATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UU-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 6-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 1-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1999
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1999
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 20-OCT 1999
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 20-OCT 1999
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/368,672
PILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                   : CIBA-GEIGY Corporation
7 Skyline Drive
Duesing, John H.
Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montcya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Steinson, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                     APPLICANT:
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                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 ATCAACCAAGCTGGTAATGGTTGCGCGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 GCGTGTGTGTCAAAGTCTCGGTCTTGACCCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
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                                                                                                                                                                                                                                                                                                                                                                                                       1079
148
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                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERNCET VONCHER: 36,129
REFERNCET VUMBER: 8-19825/P1/CGC 1727
TELECOMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8689
INFORMATION FOR SEO 1D NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-692-367-70 (1-250) x US-08-181-271A-37 (1-1079)
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830.00
73.09%
59.44%
58.95%
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                   US-08-181-271A-37
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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDERS: 106
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Fight PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/49,315
FILING DATE: 12-AM-94
APPLICATION NUMBER: US 08/181,271
FILING DATE: 15-JU-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APP-1991
PRIOR APPLICATION NUMBER: US 07/58,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION NUMBER: US 07/58,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION NUMBER: US 07/58,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: B-MAR-1988
PRIOR APPLICATION NUMBER: US 07/165,667
FILING DATE: B-MAR-1988
PRIOR APPLICATION NUMBER: US 08/042,847
                                                          FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425 EACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                       Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                               Sequence 37, Application US/08449315
Patent No. 5650505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Wares, Scott J.
Ward, Eric R.
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
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261 ATCAACCAAGCTGGTAATGGTTGCGCGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
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321 AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTACC------AGACGT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGAGGTTTCTTTAACAATATT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62
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148
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                                                         FILING DATE: 6-MAKI-1992

PRIOR APPLICATION DATA: 7-SEP-1991

APPLICATION NUMBER: US 07/768,122

PRIOR APPLICATION NUMBER: US 07/580,431

APPLICATION NUMBER: US 07/580,431

APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/368,672

PRIOR APPLICATION NUMBER: US 07/329,018

PRIOR APPLICATION NUMBER: US 07/329,018

PRIOR APPLICATION UNMBER: US 08/045,957

PRIOR APPLICATION UNMBER: 38/129

RAPLICATION NUMBER: 36,129

REGISTRATION NUMBER: 36,129

REGISTRATION NUMBER: 36,129

REFERENCE (919)541-8614

TELERPONE: (919)541-8614

TELERPONE: (919)541-8614

TELERPONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-692-367-70 (1-250) x US-08-449-315-37 (1-1079)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS: LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.846-81
830.00
73.09%
59.44%
58.95%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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Query Match:
DB:
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549 GCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608
                                                                                                                                                                              609 CCAACTGTAGCTTTCAGGTCGGGTTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                                                                                                                                                                                                                        669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA---ATGGAATGTAACGGTGGT'725
                                                                          162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                       182 AlavalvalAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
                                                                                                                                                                                                                                  202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                                                                                                                                                                                                               222 AsnProAlaGlnMetAsnAlaArgileGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
                                                                                                                                                                                                                                                                                                                                       726 AATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Neumans, Deal-March APPLICANT: Sperison, Christoph APPLICANT: Sperison, Christoph APPLICANT: Stanson, Jeffrey R. APPLICANT: Williams, Scott J. APPLICANT: Ward, Eric R. APPLICANT: Williams, Sherica C. TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS: ADDRESSE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive CITY: Hawthorne STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 6-NOV-1992
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Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Steinson, Jeffrey R.
Uknes, Scott J.
Ward, Bric R.
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Patent No. 565414
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Alexander, Danny C.
Beck, James J.
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US-08-444-803-37
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207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer
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148
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                         PRILICATION NUMBER: US 07/305,566
FILING DATE: 1-AFR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 6-APR-1992
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 0-JUN-1989
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 0-JUN-1989
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 10-JUN-1989
PRIOR APPLICATION NUMBER: US 07/368,672
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1989
PRIOR APPLICATION NUMBER: S-19825/PI/CGC 1727
TELECOMONICATION INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: S-1983
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMONICATION INFORMATION:
TELEPHONE: (919,100)
PRIOR APPLICATION NUMBER: S-19825/PI/CGC 1727
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-692-367-70 (1-250) x US-08-444-803-37 (1-1079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
UMBER: US 07/678,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.84e-81
830.00
73.09%
59.44%
58.95%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPADING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 08/181,271
FILING DATE: 3-JAN-94
APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
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REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 8-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-0340.593

PRIOR DATE: 16-UTL-1993

PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATI
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-WAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-WAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 37:
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830.00
73.09%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
MOLECULE TYPE:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluileAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrileSer 122
                                                                                                                                                                                                                                                                                                     182 AlavalvalAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 CCAACTGTAGCTTTCAGGTCGGGTTTGTGGATGAATAGCGTAAGGCCGGTTCTG 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
                                                                                                                                                                                                                                                                                                                                                                                     GlulleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 GCGTGTGGTCAAAGTCTTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 ProGinGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
                              63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 ValAspProGlyProAsnLeuThrCys 250
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STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08449043
Patent No. 568904
GENERAL INFORMATION:
APPLICANT: RYAIS, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alexander, Danny C.
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Neuhaus, Jean-Marc
Payne, George B.
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Ward, Eric R.
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COUNTRY: USA
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CITY: Ha
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APPLICANT:
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APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                        ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                     OPERATING SYSTEM:
                      New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
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                                        COUNTRY:
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                                                                                                                                                                                                                                                                                             207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                                                                          261 ATCAACCAGGTGATGGTTGCGCGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       609 CCAACTGTAGCTTTCAGGTCTTGTGGTTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlulleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GAAATTGCTACCATGTTTGCTCATTTCACTCACGAGACCGGACATTTCTGCTACATAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlulleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 GCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGGTAGCAAC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                            23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42
                                                                                                                                                                                                                                                                       43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62
                                                                                                                                                                                                                                                                                                                                                    63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIEA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                             US-10-692-367-70 (1-250) x US-08-449-043-37 (1-1079)
  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ValAspProGlyProAsnLeuThrCys 250
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US-08-456-265A-37
US-08-456-265A-37
Sequence 37, Application US/08456265A
Patent No. 5767369
GENERAL INFORMATION:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
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                    Query Match:
DB:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERBUSC JOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR DATE: 8-FART.1988
PRIOR DATE: 8-FART.1988
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APPL.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
RILING DATE: 27-58P-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 77-58P-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-58P-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
PILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR DATE:

APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APPL-1991
PRIOR APPLICATION DATE: BRICK APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
E: Floppy disk
IBM PC compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:

ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
FILING PATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/165,667
PILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-WAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991 APPLICATION DATA: APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UUN-1989
PRIOR APPLICATION DATA:
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FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
                     Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                       Moyer, Mary B.
Nehhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
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                                                                                                                                                                                                                                                                               GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGer 42
                                                                                                                                                                                                                                                                                                                                                                                                                                            43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                      1079
148
34
57
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                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                         US-10-692-367-70 (1-250) x US-08-456-265A-37 (1-1079)
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Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
                                                               830.00
73.09%
59.44%
58.95%
                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                        Alignment Scores:
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                         APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425.504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAX-1995
CLASSPETCATION: 315
RADELICATION BATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 16-UUL-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/305,566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: CIBA-GEIGY Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                ; Sequence 37, Application US/08455244
; Patent No. 5789214
                                                                                                                                                                                                                                          Alexander, Danny C.
Beck, James J.
                                                                                                                                                                                                                                                                                Duesing, John H.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                         Ryals, John A.
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                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
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US-08-455-244-37
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 AACGCCCCTAATACTTTCCCCAACTTTGCCAATTCTGTTACC-----AGACGT
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148
34
57
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATORNEY/ASERT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPRENCE/DOCKET NUMBER: 3-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8649
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDIES: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-692-367-70 (1-250) x US-08-455-416-37 (1-1079)
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Indels:
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830.00
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Friedrich, Leslie B.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Harms, Christian
APPLICANT: Harms, Christian
APPLICANT: Montoya, Alice
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Moyer, Mary B.
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Williams, Scott J.
APPLICANT: Williams, Shericca C.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHRICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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142 AlaGlyClnLysTyrTyrGlyArgClyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
                                                                                                                                                                                                                                                                                                                                                                                      242 ValAspProGlyProAsnLeuThrCys 250
                                                                                                                                                                                                                                                                                                                                                                                                          786 GTGGACCCTGGTCCTAACCTTAGTTGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NOMBER: 05/01/21.

FILING DATE: 13-7AN-94

APPLICATION NUMBER: US 08/093,301

FILING APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Beck, James J.
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Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACATTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 ATCAACCAGGTGGTAATGGTTGGGGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|||
321 AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTACC------AGACGT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlulleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SeralavalLysalaTyrProGlyPhealaHisGlyGlySerGlnValGlnGlyLysarg 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluileAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATTGCTACCATGTTTGCTCATTTCACTCAGGACGACGACATTTCTGCTACATAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079
148
34
57
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                                                                  PRIOR PELLORION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-692-367-70 (1-250) x US-08-455-244-37 (1-1079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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830.00
73.09%
59.44%
58.95%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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549 GCGTGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAGCCGAACTTGTGGGTAGCAAC 608
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                                                                                                                                                                                                                           182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
                                                                                                                                                                                                                                                                                                                                                                                                   222 AsnProAlaGlnMetAsnAlaArglleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
                                                                                     162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                                                                                                                             202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 AATTCCGGTGCAGCTAAGGATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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488

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261 ATCAACCAAGCTGGTAATGGTTGCGCGGAAAAAATTCTACACCCGTGACTCTTTCGTT 320
                                                                                                                                                                              103 GluilealaalaPhePhealaHisAlaThrHisGluThrGlyHisPheCysTyrileSer 122
                                                                                                                                                                                                       GlulleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                                                                                                                                                                                                   142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161
                                                                                                                                                                                                                                                                                                                                                                          162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 GCGTGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAAGCAAC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609 CCAACTGTAGCTTTCAGGTCTGGTTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA---ATGGAATGTAACGGTGGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet
      LysAanGlnalaGlySerGlyCysGluGlyLysAansheTyrThrArgSerAlaPheLeu
                                                                                           SeralaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                   321 AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTACC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 ValAspProGlyProAsnLeuThrCys 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              786 GIGGACCCIGGICCTAACCTTAGITGC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CIBA-GRIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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; Patent No. 5847258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-457-364-37
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT
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148
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Matches:
Conservative:
Mismatches:
Indels:
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PAPELICATION NUMBER: US 07/678,378
PRIOR DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/768,122
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-UNN-1989 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/329,018 FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.84e-81
830.00
73.09$
59.44$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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DB:
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1079
148
34
        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFFTATTAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                       CLASSIFICATION: 910
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 (191,271
FILING DATE: 16-701-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 16-701-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/65,667
FILING DATE: 6-REB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/65,667
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/65,667
FILING DATE: 20-0CT 1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/68,122
APPLICATION NUMBER: US 07/580,431
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/368,672
APPLICATION NUMBER: US 07/368,672
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/368,672
FILING DATE: 12-APR-1983
ATTORNEY APPLICATION NUMBER: US 07/368,672
FILING DATE: 12-APR-1983
ATTORNEY APPLICATION NUMBER: US 07/329,018
FILING DATE: 12-APR-1983
ATTORNEY APPLICATION NUMBER: US 07/308,672
FILING DATE: 12-APR-1983
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SEQUENCE CHARACTERISTICS.
LENGTH: 1079 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.84e-81
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REGISTRATION NUMBER: 36.
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COMPUTER READABLE FORM:
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Score:
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207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
                                                                                                                                                                                                                                                                                                                             261 ATCAACCAAGCTGGTAATGGTTGCGCGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
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                                                                                                                      93 CARARACTGCGGTTGCGCTCCARARCTCTGTTGCAGTCAGTTCGGTTACTGTGGTACCGAC 152
                                                                                                                                                                                     83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                                                                                    3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlySer
                                                                                                                                                                                                                                      43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle
 57
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                                                                  US-10-692-367-70 (1-250) x US-08-457-364-37 (1-1079)
   Mismatches:
                 Indels:
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Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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; Patent No. 5851766
59.44%
58.95%
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APPLICANT: Ryals,
 Best Local Similarity:
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US-08-456-262-37
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APPLICANT: Reshuba, Caccage B.
APPLICANT: Payer, Caccage B.
APPLICANT: Payer, Caccage B.
APPLICANT: Esperison, Officiar oph
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148
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Mismatches:
Indels:
  S-19825/P1/CGC 1727
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Matches:
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                                TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER: S.
TELECOMMUNICATION INFORMATION
TELEPHONE: (919)541-8614
                                                                                                                                                           4.84e-81
830.00
73.09%
59.44%
58.95%
                                                                                                       linear
                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-456-262-37
                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                    Alignment Scores:
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APPLICATION NUMBER:

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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
786 GIGGACCCIGGICCIAACCITAGIIGC 812
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-7AN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-7UL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APPL-1991
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 6-FEB-1989
FILING DATE: 6-FEB-1989
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 6-FEB-1993
FILING DATE: 6-REPLIPS]
FILING DATE: 12-DEC-1990
FILING DATE: 21-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
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FILING DATE: 20-OCT 1989
                                                                                                                                         Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Priedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                             Patent No. 5856154
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                 Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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Neuhaus, Jean-Marc
Payne, George B.
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                       RESULT 13
US-08-456-240-37
                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
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207 CCGACCGGAGGG-----TCGGTCGCTAGCATTGTGACACAAGGTTTCTTTAACAATATT 260
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                                                   APPLICATION UNBER: US 07/580,431
FILING DATE: 7-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUNICATION:
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Matches:
Conservative:
Mismatches:
Indels:
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JMBER: US 07/768,122
27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919)541-8614
TELEPAX: (919)541-8689
INFORMATION FOR SEQ 1D NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.84e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830.00
73.09%
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Best Local Similarity:
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                                                           609 CCAACTGTAGCTTTCAGGTCGGGTTTGTGGTTTTGGATGAATAGCCTAAGGCCGGTTCTG 668
                                                                                                549 GCGTGTGGTCAAAAGTCTCGGTCTTGACGCCAGCCCGAACTTGTGGGTAGCAAC 608
                                           182 AlavalvalAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnvalHisArgValMet 201
                                                                                                                                                    AsnProAlaGlnMetAsnAlaArgileGlyTyrTyrLysGlnTyrCysArgGlnLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,736

FILNG DATE: 11—AAY 1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/08/12/11

APPLICATION NUMBER: US/08/13/11

FILING DATE: 13—JAN-1994

APPLICATION NUMBER: US 07/93/19/11

FILING DATE: 16—JUL-1993

PRIOR APPLICATION NUMBER: US 07/93/19/7

FILING DATE: 6—NOV-1992

PRIOR APPLICATION NUMBER: US 07/93/19/7

FILING DATE: 1—PH-1991

PRIOR APPLICATION NUMBER: US 07/93/19/7

PILING DATE: 1—PH-1991

PRIOR APPLICATION NUMBER: US 07/678,378

PILING DATE: 1—PH-1991

PRIOR APPLICATION NUMBER: US 07/505,566
                                                                                                                                                                                                               242 ValAspProGlyProAsnLeuThrCys 250
                                                                                                                                                                                                                             786 GIGGACCCIGGICCTAACCITAGITGC 812
                                                                                                                                                                                                                                                                                                                                     Alexander, Danny C.
Beck, James J.
Puesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             Sequence 37, Application US/08455736 Patent No. 5880328
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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261 ATCAACCAAGGTGATAGGTTGCGCGGGGAAAAGATTCTACACCCGTGACTCTTTCGTT 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyIle 62
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 6-ARL-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-40M-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 20-40M-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIMEY, James SCOCT

REFERENCE/DOCKET NUMBER: 36,129

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIMEY, James SCOCT

REFERENCE/DOCKET NUMBER: 36,129

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

TELEPHONE: (919)541-8689

INFORMATION FOR SED ID NO: 37:

SEQUENCE CHARACTERISTICS:

**CHARACTERISTICS:

**CHARACTERISTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
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73.09%
59.44%
58.95%
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STRANDEDNESS: single
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Best Local Similarity:
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                       549 GCGTGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCGAACTTGTGGGTAGCAAC 608
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SeralavalLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
                                                                        GluIleAlaAlaPheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
                                                                                                                                               GlulleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                       162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 ProginglyPheGlyAlaThrileArgAlaileAsnGlyAlaLeuGluCygAspGlyAsn 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 AATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGAGACTATTGTGGACAGCTTGGT 785
                                                                                                                                                                           142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly
                                                                                                                                                                                                                                                  489 CCGGGAAAAGGCTACTTCGGTCGTGGTCCGATCCAACTATCATGGAACTACAACTACGGA
                                                                                                                                                                                                                                                                                                                                                                              182 AlavalvalAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgvalMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08971217

Sequence 37, Application US/08971217

Patent No. 5942662

GENERAL INFORMATION:

APPLICANT: Ryals, John A.

APPLICANT: Friedrich, Leslie

APPLICANT: Beck, James

APPLICANT: Ward, Eric

SCOTT

APPLICANT: Ward, Eric

APPLICANT: Ward, Eric

STREET: 3054 Cornwall:

CTREET: 3054 Cornwall:

STREET: 3054 Cornwall:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3054 Cornwallis Road, P.O. Box 1257 CITY: Research Triangle Park STATE: NC COUNTRY: USA ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 ValAspProGlyProAsnLeuThrCys 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-DAN-1994
PRIOR APPLICATION NUMBER: US 08/181,271
APPLICATION NUMBER: US 08/002 10-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-971-217-37
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GATGCATACTGCGGGTGTTGGATGCCGATCAGGTCCTTGTAGA-----GGTAGTGGAACC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timochy
REGISTATION NUMBER: 38,241
REGISTATION NUMBER: 8-19825/PI/CGC 1727/DIV5/CONT
TELECOMMUNICATION INFORMATION: 7FLEPHONE: (919)541-8587
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1079
148
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-692-367-70 (1-250) x US-08-971-217-37 (1-1079)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

PRIOR APPLICATION DATE:

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991

PRIOR APPLICATION NUMBER: US 07/560,431

FILING DATE: 7-SEP-1991

PRIOR APPLICATION NUMBER: US 07/560,431

FILING DATE: 20-UN-1989

PRIOR APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-UN-1989

PRIOR APPLICATION NUMBER: US 07/368,672

FILING DATE: 24-MAR-1989

PRIOR APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION NUMBER: US 08/45,957

FILING DATE: 12-APR-1983

ATTORNEY AMERICATION NUMBER: US 08/45,957

FILING DATE: 12-APR-1983

ATTORNEY AMERICATION NUMBER: US 08/45,957

FILING DATE: 12-APR-1983
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207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTAGAGGTTTCTTAACAATATT 260
                                      321 AACGCCGCTAATACTTTCCCCAACTTTGCCAATTCTGTTACC------AGACGT 368
                                                                                                                                                           GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
                                                                                                                                                                       162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
                                                                                                                                                                                                                                                        549 GCGTGTGGTCAAAAGTCTCGGTCTTGACGCCAGCCCGAACTTGTGGGTAGCAAC 608
                                                                                                                                                                                                                                                                                   182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
                                                                                                                                                                                                                                                                                                609 CCAACTGTAGCTTTCAGGTCGGGTTTTTGGATGAATAGCGTAAGGCCGGTTCTG 668
                                                                                                                                                                                                                                                                                                                           202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
                                                                                                                                                                                                                                                                                                                                        669 AACCAAGGTTTGGAGCCACCATTAGAGCTATTAATGGA---ATGGAATGTAACGGTGGT 725
                                                                             SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
62
SerGlyGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                           ValAspProGlyProAsnLeuThrCys 250
43
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Search completed: May 23, 2005, 20:45:52 Job time : 131.74 secs

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Sequence:

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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.lastate.edu; TIGR,
www.ligr.org; or NNEI, www.ncbi.nlm.nih.gov. When the source of the
maize CDNA sequences is either Virginia Malbot, Stanford or Pat
Schnable, lowa State, then clones may be requested from ZmDB:
www.zmdb.lastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 1179)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Arthur, L.W., Hanafey, M., Consensus Sequences for Design of Overgo Probes
Unpublished (2002)

2 (bases 1 to 1179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                       CB981043
CB980332
CB982059
                                                    CD994869
CD994156
                                                                                                                                                                                                                                       CB981065
CB982079
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CB980773
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CD995176
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1. 1179
/organism="Zea mays"
                                                                                                                                                                                                      CN132942
                                                                                                                                                                                                                                                                                                                                     CB981568
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Zea mays
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-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US10692367/runat_20052005_172255_20018/app_query.fasta_1.846
-D=/cgn2_1/USPTO_spool/US10692367/runat_20052005_172255_20018/app_query.fasta_1.846
-DB=ST_QFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNTS-bits -START=1 -RND=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNTFMT=ptc - NORM==xt -HEAPSIZES=500 -MINLENS - MATRIX=200000000
-USRE-US10692367_@CGN_1 1_3556_@runat_2052051_72255_20018 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DBV TIMBOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPEXT=7
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BGB37663 Zml0 01e1
CD435649 EL01N0364
BGB3747 Zml0 10h0
CO524416 3530 1 16
CN133023 OX1 9 D11
CD443492 EL0IN0427
CA197556 SCBFAD106
BM736454 952051A06
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                                                                                                                          // Search time 2237.67 Seconds
(without alignments)
4252.663 Million cell updates/sec
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                                                                                                                                                                                                                                         SMQNCGCQPNVCCSKFGYCG.....GYYKQYCRQLGVDPGPNLTC 250
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                             34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BGB37663
CD435649
BGB37479
CO524416
CN133023
CD443492
CA197556
BM736454
                                                                                                                              23, 2005, 17:04:03
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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DB seq length: 200000000
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Match Length DB
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Perfect score:
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1099.5
1062.5
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Database :

Result Š.

HTC 16-0CT-2002

CAB70004 CAB70003 CAB70002 CAB70005 CAB70003 RR890915N

RR89015NO

Total number

Minimum I Maximum I

QBB20hil: PUFQC18TB CAB70003 CAB70003 OV1 8 G11 SCCCCL700 QBG4f06.x

QBG10a02. QBG11a02.

CAB70005 CAB70004 CAB70005 CAB70003

CG328450 CD328450 CD328450 CD394885 CD395437 CD395437 CD395437 CD395437 CD395437 CD395454 CM132942 CM132942 CM132942 CM132942 CM132942 CM3961065 CM3961065 CM3961073 C

QBB18e05. QBB25f07. QBB13e04. SCAGSD104 QBB15f08. WOUND1 75 OX1 9 D11 3530 1 13

869 TACTGCCAGCAGCTCCGCGTCGACCCAGGGCCCAACCTCACTTGC 913

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/note="Vector: Bluescript SK+/Xhol-EcoRI; Site 1: EcoRI; Site 2: Xhol; Field-grown corn was silk channeI-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG837663 855 bp mRNA linear EST 25-MAY-2001
Zml0_01e10_A Zml0_AAFC_ECORC_Fusarium_graminearum_corn_silk Zea
mays cDNA clone Zml0_01e10, mRNA sequence.
                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 855)
Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A, Sprott, D. and Tinker, N.A.

Expressed Sequence Tagg from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794 CAGTCGGGCCCGTC-CGCTCGGCGGCGGCGGCAGTGGCGGCGCGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AlaSerValValThrGlySerPhePheAsnGlyIleLy8AsnGlnAlaGlySerGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 GCTAGCGTCGTCACCGCTCCTTCTTCAACGCATCAAGAGCCAGGCCGGGAGCGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GlnSerGlyProCysArgSerGlyGlyGlyGlyGlySerSerGlyGlyGlyGlyAlaAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualifiers
                                                                                                                                                   BG837663.1 GI:14203986
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Zea mays
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VERSION
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SOURCE
ORGANISM
                                       RESULT 2
BG837663/c
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                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 AACAGGGGGGGAGGACGCGGGATCGCGTTCAAGACGGCGCTCTGGTTCTGGATGAAC 748
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                                                                                        Incre—"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 GGACATTICTGCTACATCAGCGAGATCAACAAGAGGAACGCCTACTGCGACGCGAGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 AGGCAGTGGCCGTGCGCGGCGGGCAGAAGTACTACGGGCCCGGCCCCGCTGCAGATCTCG
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222
13
13
1
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Matches:
Conservative:
Mismatches:
Indels:
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|db_xref="MaizeDB:638921"
|db_xref="taxon:4577"
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92.16%
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ZM10_10h09_A ZM10_AAFC_ECORC_FUSArium_graminearum_corn_silk Zeamays cDNA_clone Zm10_10h09, mRNA sequence.
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Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCGCAGGTGCAGGGCAAGCGC
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                                                                                                                                                         AlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyr 130
                                                                                                                                                                                                                                                                                                                          GluGlyLysAanPheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGly 90
                                                                                                                       557
                                                                                                                                                                                                                                          CyshapproThrLyshrgGlnTrpProCyshlaAlaGlyGlnLysTyrTyrGlyArgGly 150
                                                                                                                                                                                                                                                                                                                                                                                                         GlyLeuGlyAspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeu 190
                                                                                                                                                                                                                                                                                                                                                                                                                                AlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArglle 230
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1 (bases 1 to 737)
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.

Comparison of the maize endosperm transcriptome and its Genome Res. 14 (10), 1932-1937 (2004)
                                                                            PheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHis 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD435649 737 bp mRNA linear EST
EL01N0364B04.b Endosperm_3 Zea mays CDNA, mRNA sequence.
CD435649
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Makeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ
Tel: 732-445-3801
Fax: 732-445-5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jlai@waksman.rutgers.edu
Seq primer: T3.
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//dev_bote="multiple"
//dev_bote="multiple"
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Invitrogen from multiple tissues"
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Inote="Organ: silks, husks, ears, pollen, shoot tips,
Inote="forgan: silks, husks, ears, pollen, shoot tips,
Inote: for tips, whole seed, embryo; Vector: pCNV-SPORT
6.1; Site=1: BCORY; Site=2: Not1; Maize Gene Discovery
Froject contracted with Invitrogen to produce a
normalized, full length library in a pSport vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
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3530 1 161 1 E12.y 1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bepernatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         691 CAACGGGAACAACCCCGCCCAGATGAACGCGCGGTCGGCTACTACAAGCAGTACTGCCA 750
                                                                                   GCCGTGCGCGGCGGCGCAGAAGTACTACGGGCGCGGCCCGCTGCAGATCTCGTGGAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                          158 rAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgVa
                                                                                                                                                                             511 CAACTACGGGCCCGCCGGGAGGGACATCGGCTTCAACGGGCTCGCCGACCCCAACAGGGT
                                                                                                                                                                                                                                            178 lalaargaspalavalvalalapheLysalaalaLeuTrpPheTrpMetAsnAsnValHi
                                                                                                                                                                                                                                                                                                                                            198 sArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCy
                                                                                                                                                                                                                                                                                                                                                                                          631 CCGTGTGATGCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTG
                                                  138 pProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTy
                                                                                                                                                                                                                                                                                          571 GCGCAGGACGCCGTGATCGCGTTCAAGACGGCGCTCTGGTTCTGGATGAACAACGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Are, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 3530 1 161 1 row: B column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Walbot V
Department of Biological Sciences
Stanford University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_st_gg="4-5 days post-silk emergence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGACGACTACTGCGGCGACGGGTGCCAGTCGGGCCCCGTSCGCTCGGGCGGCGSCGGCGS 151
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                           ğ
          Harris, L. J. Balcerak, M., Allard, S., Saparno, A., Couroux, P., Moors, A., Hattori, J. I., Ouellet, T., Robert, L. S., Singh, J. A., Sprott, D. and Tinker, N. A.

Sprott, D. and Tinker, N. A.

Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum

Unpublished (2001)

Contact: Harris, Linda J.

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada

Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
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Mismatches:
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tissue_type="Silk"
                                                                                                                                                                                                                                                                                       Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualifiers
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mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5. cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm, 5. 2 mm to 2 cm ears; 6. pollen; 7..1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 2 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery Ext sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (http://www.genome.arizona.edu/orders/). High density filters containing over 18,1000 clones can also be ordered from the University of Arizona.

547 GGGCAGAAGTACTACGGGCGCGCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCC 606 999 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro 202 187 GACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGTGCCGCTCGGGCGGCGGCGGCGCAGC 246 307 AAGAGCCAGGCGGAGCGGGTGCGAAGAACTTCTACACCCGGAGCGCGTTCCTG 366 427 GAGATCGCCGCCTTCTTCGCGCACGCCACGCACGAGACCGGGCATTTCTGCTACATCAGC 486 GluIleSerLygSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAla 142 546 | GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro 162 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182 726 247 AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCACCGGCTCCTTCTTCAACGGCATC 306 367 AGCGCCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCGCAGGTGCAGGGCAAGGCA GluileAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlySer 42 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu,82 GladenCysGlyCysGlaprodenValCysCysSerLysPheGlyTyrCysGlyThrThr 487 GAGATCAACAAGAGCAACGCCTACTGCGACCAGAGAAGAGGCAGTGGCCGTGCGCGG GCGGGGAGGCCATCGGCTTCGACGCTCGGGGACCCCCGGCAGGGTGGCTCGGGAACCCCC GTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGGTGGTGCCG 767 206 4 0 Length:
Matches:
Conservative:
Mismatches: (1-767)US-10-692-367-70 (1-250) x CO524416 6.96e-109 1160.00 98.59% 96.71% 82.39% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: m 23 43 143 163 607 183 299 63 83 103 123 Pred. No.: g ò ò g ò 셤 ઠે g ሯ 요 ò g 8 g è g ð ઠે 셤

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/db xref="taxon:458" / db xref="taxon:4588" / clone="0X1 9 Dil A002" / clone="0X1 9 Dil A002" / clone="0X1 9 Dil A002" / clone lib="0xidatively-garrensed leaves and roots" / clone lib="0xidatively-garrensed leaves and roots" / clone lib="0xidatively-garrensed leaves and roots" / note="organ: Leaf and Root; Vector: pWE188-FL3; Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DralII sites of the pWE188-FL3 vector (5-prime DralII site is GACTGTGG, 3-prime_DralII site is CACTGTGG).
                                                                                                                                                    CN133023

OX1 9 D11.g1 A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1 9 D11 A002 5', mRNA sequence.

CN133023.1 GI:45963543
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Vutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science, plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polya.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

(Dases 1 to 837)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
Unpublished (2003)
Other ESTs: OXI 9 D11.bl A002
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fal: 706 542 1860
Fax: 706 583 0210
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/organism="Sorghum bicolor"
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/cultivar="BTx623"
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Saccharum officinarum
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(Labase 1 to 710)

Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F., Larkins,B., Becraft,P. and Messing,J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
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                                                                                                     LysAsnGlnAlaClySerGlyCysGluGlyLysAsnPhsTyrThrArgSerAlaPhsLeu
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 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr
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Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghnysen RG., Fiscataway, NJ
Tel: 732-445-5380
Frax: 732-445-5735
Email: jlai@waksman.rutgers.edu
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AUTHORS
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297 GCCTACTGCGACTCGAGCAACAGGCAGTGGCCGGGGCGGGGGCAGAAGTACTACGGG 356
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/organism="Zea mays"
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Unpublished (1999)
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//one="Organ: seedlings inoculated with Gluconacetobacter
diazotroficans; Vector: pSport1; Site 1: Sal1; Site 2:
diazotroficans; Vector: pSport1; Site 1: Sal1; Site 2:
Not1; An unidirectional cDNA library generated from
[seedlings inoculated with Gluconacetobacter
diazotroficans]. CDNA was prepared from poly4+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kw were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                      E Ubases 1 to 647)
S Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
L Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 067 row: A column: 11
Seq primer: T7 Promoter Primer.
Seq primer: T7 Promoter Primer.
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/organism="Saccharum officinarum"
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Matches:
Conservative:
Mismatches:
Indels:
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/clone="SCBFAD1067A11"
/lab host="DH10B"
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Best Local Similarity:
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fincte-"vector: pUC19; Site 1: ECORI; Site 2: ECORI; The library was prepared by George Rudenko using poly (A) elected RNA and Universal Ribochone CDNA Synthesis System (Promes). CDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with ECORI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into ECORI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover 228 169 PheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValValAlaPheLysAla 188 208 536 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. BM736454 1 10-2 628 bp mRNA linear EST 01-MAR-20 952051A06.xl 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea 209 IleArgAlaIleAsnGlyAlaLeuGluCy8AspGlyAsnAsnProAlaGlnMetAsnAla 477 ececrcregricregaceaacaacerececeserearercecaeceaeceaec 149 ArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGly 189 AlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThr /clone_lib="952 - BMS tissue from Walbot Lab (reduced /mol_type="mRNA" | /cultivar="BMS (Black Mexican Sweet)" | /db_xref="taxon:4577" | /tisuce_type="euspension culture" | /dev_stage="mixed logarithmic and stationary growth phases" Maize BSTs from various cDNA libraries sequenced at Stanford Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 952051 row: A column: 06.

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Jibrary was prepared by George Rudenko using poly (A) library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone CDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo (dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUCI9 vector. Blue/white selection on carbenicillin-containing plates was used to recover
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                                                                                                                                                                                                                                                                                                                           /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
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|/cultivat==BMS (Black Mexican Sweet)"
|/db_xref="taxon:4577"
|/tissue type="suspension culture"
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Matches:
Conservative:
Mismatches:
Indels:
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               855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8227
Email: walbot@stanford.edu
Plate: 952073 row: H column: 05
Location/Qualifiers
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952073H05.yl 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
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clade, Panicoideae, Andropogoneae, Zea.
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Department of Biological Sciences
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Saccharum officinarum
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
Slade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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123 lulleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaG 143
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 051 row: P column: 10
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                         533 GGCAGAAGTACTACGGGCGCGGCCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCG
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    /organism="Saccharum officinarum"

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The libraries that made SUCRST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 978)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Uppublished (2002)
Coher GSSs: GG3CW08TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:4577"
/clone="ZWBMa0778B15"
/clone lib="ZM 0.7 l15_KB"
/note="Wetcor: pBGSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 741)

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Matches:
Conservative:
Mismatches:
Indels:
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Unpublished (2003)
Contact: Genoplante
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                                                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                 CD994869.1 GI:32855188
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975.00
97.81%
94.54%
69.25%
   AGGAAACAACCC 783
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Best Local Similarity:
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DB:
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AUTHORS
TITLE
JOURNAL
COMMENT
                                   RESULT 13
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growing in greenhouse; Vector: BSport1; Site 1: Sal1;
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from [Lateral buds from plants adult plants growing in
greenhouse]. CDNA was prepared from poly4- mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Matches:
Conservative:
Mismatches:
Indels:
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978.00
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69.46%
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bp mRNA linear EST 16-JUL-2003
clone QBB18e05, mRNA sequence.
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                                                                                                                                                                                                                                                              227 AsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyPro 246
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomics
147 TyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAsp
                                                                                              167 IleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValValAlaPhe
                                                                                                                                                    LysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGly
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Contact: Genoplante
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Matches:
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Mismatches:
Indels:
Gaps:
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QBB18605.xg QBB Zea mays cDNA
CD994885
CD994885.1 GI:32855204
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971.00
97.27%
93.99%
68.96%
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Best Local Similarity:
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Pred. No.:
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DB:
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AUTHORS
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                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Contact: Genoplante
Genoplante
Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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97.28%
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Zea mays
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Pred. No.:
                                          208
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TyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLy8argGluIleAlaAlaPhe 107
                                            GlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAlaPheLys 187
                                                                                                                                  101 GCCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGGGACGCCGTGGTGGCGTTCAAG 360
                                                                                                                                                  AlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAla 207
                                                                                                                                                          361 GCGGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGGTGGTGCCCCAGGGGTTCGGCGCC 420
                                                                                                                                                                           ThrileArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsn 227
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LeuThrCys 250
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